



Db 18 DFGLDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGCEF-----VFLQKY 72

QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109

Db 73 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 126

RESULT 2

US-09-177-860A-6

; Sequence 6, Application US/09177860A

; Patent No. 6096506

; GENERAL INFORMATION:

; APPLICANT: Huynh, Thanh

; APPLICANT: Lee, Se-Jin

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Gray Cary Ware & Freidenrich LLP

; STREET: 4365 Executive Drive, Suite 1600

; CITY: San Diego

; STATE: CA

; COUNTRY: US

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/177,860A

; FILING DATE: 23-OCT-1998

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/525,596

; FILING DATE: 19-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Ph.D, Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/075003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 858-677-1456

; TELEFAX: 858-677-1465

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 126 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-09-177-860A-6

Query Match 80.4%; Score 501; DB 3; Length 126;

Best Local Similarity 80.7%; Pred. No. 6.7e-52;

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGCEFNFTVSFWLRY 60

Db 18 DFGLDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGCEF-----VFLQKY 72

QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109

Db 73 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 126

RESULT 3

US-09-378-238-6

; Sequence 6, Application US/09378238

; Patent No. 6465239

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; APPLICANT: McPherron, Alexandra C.

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC

; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES

; FILE REFERENCE: JHU1120-9

; CURRENT APPLICATION NUMBER: US/09/378,238

; CURRENT FILING DATE: 1999-08-19

; EARLIER APPLICATION NUMBER: 08/795,071

; EARLIER FILING DATE: 1997-02-05

; EARLIER APPLICATION NUMBER: 08/525,596

; EARLIER FILING DATE: 1995-10-25

; EARLIER APPLICATION NUMBER: PCT/US94/03019

; EARLIER FILING DATE: 1994-03-18

; EARLIER APPLICATION NUMBER: 08/033,923

; EARLIER FILING DATE: 1993-03-19

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 126

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-378-238-6

Query Match 80.4%; Score 501; DB 4; Length 126;

Best Local Similarity 80.7%; Pred. No. 6.7e-52;

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGCEFNFTVSFWLRY 60

Db 18 DFGLDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGCEF-----VFLQKY 72

QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109

Db 73 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 126

RESULT 4

US-09-451-501-6

; Sequence 6, Application US/09451501

; Patent No. 6468535

; GENERAL INFORMATION:

; APPLICANT: Se-Jin Lee et al.,

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/451,501

; FILING DATE: 30-NO. 6468535-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/795,071

; FILING DATE: <Unknown>

; APPLICATION NUMBER: PCT/US94/03019

; FILING DATE: 18-March-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lisa A. Haile, Ph.D.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/105001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 126 amino acids

; TYPE: amino acid



Query Match 80.4%; Score 501; DB 2; Length 375;  
Best Local Similarity 80.7%; Pred. No. 2.5e-51;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFNNFTVSFWLRY 60  
|||||  
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECF-----VFLQKY 321

QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIIGKIPAMVYDRGCGS 109  
|  
Db 322 PHTHLVHQANPRGSAGPCCPTPTKMSPINMLYFNKGKQIIGKIPAMVYDRGCGS 375

RESULT 8  
US-08-765-875-5  
; Sequence 5, Application US/08765875  
; Patent No. 5914234  
; GENERAL INFORMATION:  
; APPLICANT: LEE, SE-JIN  
; APPLICANT: MCPHERRON, ALEXANDRA C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
; CITY: LOS ANGELES  
; STATE: CALIFORNIA  
; COUNTRY: US  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,875  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/706,958  
; FILING DATE:  
; APPLICATION NUMBER: US/08/272,763  
; FILING DATE: 08-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TUMARKIN PH.D., LISA A.  
; REGISTRATION NUMBER: P-38,347  
; REFERENCE/DOCKET NUMBER: PD3641  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/455-5100  
; TELEFAX: 619/455-5110  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; IMMEDIATE SOURCE:  
; CLONE: GDF-8  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..375  
; US-08-765-875-5

Query Match 80.4%; Score 501; DB 2; Length 375;  
Best Local Similarity 80.7%; Pred. No. 2.5e-51;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFNNFTVSFWLRY 60  
|||||  
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECF-----VFLQKY 321

QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIIGKIPAMVYDRGCGS 109  
|  
Db 322 PHTHLVHQANPRGSAGPCCPTPTKMSPINMLYFNKGKQIIGKIPAMVYDRGCGS 375

RESULT 9  
US-08-795-671-5  
; Sequence 5, Application US/08795671  
; Patent No. 6008434  
; GENERAL INFORMATION:  
; APPLICANT: Se-jin Lee and Alexandra Mcpherron  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,671  
; FILING DATE: February 6, 1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HAILE, PH.D., LISA A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07265/106001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; IMMEDIATE SOURCE:  
; CLONE: GDF-8  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..375  
; US-08-795-671-5

Query Match 80.4%; Score 501; DB 3; Length 375;  
Best Local Similarity 80.7%; Pred. No. 2.5e-51;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFNNFTVSFWLRY 60  
|||||  
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECF-----VFLQKY 321

QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIIGKIPAMVYDRGCGS 109  
|  
Db 322 PHTHLVHQANPRGSAGPCCPTPTKMSPINMLYFNKGKQIIGKIPAMVYDRGCGS 375

RESULT 10  
US-09-177-860A-14  
; Sequence 14, Application US/09177860A  
; Patent No. 6096506  
; GENERAL INFORMATION:  
; APPLICANT: Huynh, Thanh  
; APPLICANT: Lee, Se-jin  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:



ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,860A  
FILING DATE: 23-OCT-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/525,596  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/075003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-677-1456  
TELEFAX: 858-677-1465  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-177-860A-14

Query Match 80.4%; Score 501; DB 3; Length 375;  
Best Local Similarity 80.7%; Pred. No. 2.5e-51;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
|||||  
DB 267 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECF-----VFLQKY 321  
|||||

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFKGKEQIITGKIPAMVVDRCGCS 109  
| | | | |  
DB 322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFKGKEQIITGKIPAMVVDRCGCS 375  
| | | | |

RESULT 11  
US-09-252-149B-29  
Sequence 29, Application US/09252149B  
Patent No. 6369201  
GENERAL INFORMATION:  
APPLICANT: Barker, Christopher A.  
APPLICANT: Morsey, Mohamad  
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN  
FILE REFERENCE: 9001-0042  
CURRENT APPLICATION NUMBER: US/09/252,149B  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: 60/075,213  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-252-149B-29

Query Match 80.4%; Score 501; DB 4; Length 375;  
Best Local Similarity 80.7%; Pred. No. 2.5e-51;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
|||||  
DB 267 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECF-----VFLQKY 321  
|||||

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFKGKEQIITGKIPAMVVDRCGCS 109  
| | | | |  
DB 322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFKGKEQIITGKIPAMVVDRCGCS 375  
| | | | |

RESULT 12  
US-09-252-149B-32  
Sequence 32, Application US/09252149B  
Patent No. 6369201  
GENERAL INFORMATION:  
APPLICANT: Barker, Christopher A.  
APPLICANT: Morsey, Mohamad  
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN  
FILE REFERENCE: 9001-0042  
CURRENT APPLICATION NUMBER: US/09/252,149B  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: 60/075,213  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Sus scrofa  
US-09-252-149B-32

Query Match 80.4%; Score 501; DB 4; Length 375;  
Best Local Similarity 80.7%; Pred. No. 2.5e-51;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
|||||  
DB 267 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECF-----VFLQKY 321  
|||||

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFKGKEQIITGKIPAMVVDRCGCS 109  
| | | | |  
DB 322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFKGKEQIITGKIPAMVVDRCGCS 375  
| | | | |

RESULT 13  
US-09-252-149B-34  
Sequence 34, Application US/09252149B  
Patent No. 6369201  
GENERAL INFORMATION:  
APPLICANT: Barker, Christopher A.  
APPLICANT: Morsey, Mohamad  
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN  
FILE REFERENCE: 9001-0042  
CURRENT APPLICATION NUMBER: US/09/252,149B  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: 60/075,213  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 34  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Gallus gallus  
US-09-252-149B-34

Query Match 80.4%; Score 501; DB 4; Length 375;  
Best Local Similarity 80.7%; Pred. No. 2.5e-51;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
|||||  
DB 267 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECF-----VFLQKY 321  
|||||





Db 73 PHTLVHQANPRGSAGAPCCPTFKNSPINMLYFNKGKEQILYGIKIPAMVVDRCGCS 126

## RESULT 2

```

US-09-859-211-33
; Sequence 33, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-859-211-33

```

```
query Match      80.48;  Score 501;  DB 9;  Length 130;
```

Best Local Similarity	80.7%;	Pred. No. 1.7e-43;
Matches	92; Conservative	1; Mismatches 11; Indels 10; Gaps 2;

```
QY      1  DFLDLCDEHSTESRCRPLTVDFEAFGWDWIAPKRYKANYCSGECEFFNNFTVSEWILRY 600
        |||||
        22 DFLDLCDEHSTESRCRPLTVDFEAFGWDWIAPKRYKANYCSGECEFF-----VFLQKY 760
        |||||
```

```
QY      61 PKVSASHL-----EAGPCCPTPKRSPINMLYENGKEQIITYGKIPAMVVDRCGS 109
        | |||||
DB      77 PHTHLVHQANPRGSAGAPCCPTPKRSPINMLYENGKEQIITYGKIPAMVVDRCGS 130
```

### RESULT 3

```

US-09-859-211-35
; Sequence 35, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18

```

```

; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Gallus gallus
;
US-09-859-211-35

```

Query Match	80.48;	Score 501;	DB 9;	Length 226;
-------------	--------	------------	-------	-------------

Best local similarity	80.7%;	Pred. No. 3e-43;			
Matches	92;	Conservative 1;	Mismatches 11;	Indels 10;	Gaps 2;

QY 1 DFGLDCEHSTESRCRRPLYVDFFAAGWDIIAPKRYKANCSGECEFNFTVSEFLRV 60  
| | | | | | | | | | | | | | | | | | :  
| | | | | | | | | | | | | | | | | |  
Db 118 DFGLDCEHSTESRCRRPLYVDFFAAGWDIIAPKRYKANCSGECE-----VFLOKY 172

Qy	61	PKVSASHL-----EAGPCCPTPKMSPINMLYFNGKEQLTYGKIIPAMVVDRCGCs	109
Db	173	PHTHLVHQANPRGSAGAPCCPTPKMSPINMLYFNGKEQLTYGKIIPAMVVDRCGCs	226

## RESULT 4

```

US-09-841-730 8
; Sequence 8, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-841-730-8

```

Query Match 80.48; Score 501; DB 9; Length 374;

Best Local Similarity 80.7%; Pred. No. 4.9e-43;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2.

QY    1 DFGLDCEHSEHSRCCRYPLTVDFEAFGMDWIIAPKRYKANCSGECEFNNFTVSFWLRY 60  
      | | | | | | | | | | | | | | | | | | | | :  
Db    266 DFGLDCEHSEHSRCCRYPLTVDFEAFGMDWIIAPKRYKANCSGECEF----VFLQKY 320

```
QY      61 PKVSASHL-----EAGPCCPTPKNSPINMLFYNGKEQLITGKIPAMVVDRCGS 109
        |   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     321 PHTHLVHQANPRGSAGAPCCPTPKNSPINMLFYNGKEQLITGKIPAMVVDRCGS 374
```

## RESULT 5

```

US-09-841-730-2
; Sequence 2, Application US/09841730
; Patent No. US20020157126A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Lee, Se-Jin
;
; APPLICANT: McPherron, Alexandra C.
;
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
;
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

```



```
; FILE REFERENCE: JH01470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-730-2
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Query Match      80.4%; Score 501; DB 9; Length 375;
Best Local Similarity 80.7%; Pred. No. 4.9e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
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OY 1 DEGLDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFNFTVSWLRV 60
    |||||||
Db 267 DEGLDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFNFTVSWLRV 60
    |||||||
OY 61 PKVSASHL-----EAGPCCPTPTKMSPIINMLYFNKGKQIITGKIPAMVVDRCGCS 109
    |
Db 322 PHTHLVHQANPRGSAGPCCPTPTKMSPIINMLYFNKGKQIITGKIPAMVVDRCGCS 375
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RESULT 6
US-09-841-730-14
; Sequence 14, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JH01470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Porcine
US-09-841-730-14
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Query Match      80.4%; Score 501; DB 9; Length 375;
Best Local Similarity 80.7%; Pred. No. 4.9e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
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OY 1 DEGLDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFNFTVSWLRV 60
    |||||||
Db 267 DEGLDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFNFTVSWLRV 60
    |||||||
OY 61 PKVSASHL-----EAGPCCPTPTKMSPIINMLYFNKGKQIITGKIPAMVVDRCGCS 109
    |
Db 322 PHTHLVHQANPRGSAGPCCPTPTKMSPIINMLYFNKGKQIITGKIPAMVVDRCGCS 375
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```
RESULT 7
US-09-841-730-18
; Sequence 18, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JH01470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-841-730-18
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Query Match      80.4%; Score 501; DB 9; Length 375;
Best Local Similarity 80.7%; Pred. No. 4.9e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
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OY 1 DEGLDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFNFTVSWLRV 60
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Db 267 DEGLDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFNFTVSWLRV 60
    |||||||
OY 61 PKVSASHL-----EAGPCCPTPTKMSPIINMLYFNKGKQIITGKIPAMVVDRCGCS 109
    |
Db 322 PHTHLVHQANPRGSAGPCCPTPTKMSPIINMLYFNKGKQIITGKIPAMVVDRCGCS 375
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RESULT 8
US-09-859-211-14
; Sequence 14, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-211-14
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Query Match 80.4%; Score 501; DB 9; Length 375;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
DB 267 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 109  
DB 322 PHTHLVHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 375

## RESULT 9

US-09-859-211-23  
; Sequence 23, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:

; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-859-211-23

Query Match 80.4%; Score 501; DB 9; Length 375;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
DB 267 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 109  
DB 322 PHTHLVHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 375

## RESULT 10

US-09-859-211-27  
; Sequence 27, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:

; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Meleagris gallopavo  
US-09-859-211-27

Query Match 80.4%; Score 501; DB 9; Length 375;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
DB 267 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 109  
DB 322 PHTHLVHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 375

## RESULT 11

US-09-859-211-29  
; Sequence 29, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:

; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Porcine  
US-09-859-211-29

Query Match 80.4%; Score 501; DB 9; Length 375;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
DB 267 DFGDCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109  
|  
Db 322 PHTHLVHOANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 375

RESULT 12  
US-09-454-540-5  
; Sequence 5, Application US/09454540  
; Patent No. US20010053358A1

; GENERAL INFORMATION:  
; APPLICANT: Se-Jin Lee and Alexandra McPherron

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: California

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/454,540

; FILING DATE: 06-DEC-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/795,671

; FILING DATE: February 6, 1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: HAILE, PH.D., LISA A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/106001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 375 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; IMMEDIATE SOURCE:

; CLONE: GDF-8

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..375

; US-09-454-540-5

Query Match 80.4%; Score 501; DB 10; Length 375;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRY 60  
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Db 267 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109  
|  
Db 322 PHTHLVHOANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 375

RESULT 13

US-09-841-730-4

; Sequence 4, Application US/09841730

; Patent No. US20020157126A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; APPLICANT: McPherron, Alexandra C.

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,

; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

; FILE REFERENCE: JHU1470-2

; CURRENT APPLICATION NUMBER: US/09/841,730

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: 09/626,896

; PRIOR FILING DATE: 2000-07-27

; PRIOR APPLICATION NUMBER: 09/485,046

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: PCT/US98/15598

; PRIOR FILING DATE: 1998-07-28

; PRIOR APPLICATION NUMBER: 60/054,461

; PRIOR FILING DATE: 1997-08-01

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: FastSeq for windows Version 4.0

; SEQ ID NO 4

; LENGTH: 376

; TYPE: PRT

; ORGANISM: Mus musculus

; US-09-841-730-4

Query Match 80.4%; Score 501; DB 9; Length 376;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRY 60  
|  
Db 268 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 322

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109  
|  
Db 323 PHTHLVHOANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 376

RESULT 14

US-09-841-730-6

; Sequence 6, Application US/09841730

; Patent No. US20020157126A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; APPLICANT: McPherron, Alexandra C.

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,

; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

; FILE REFERENCE: JHU1470-2

; CURRENT APPLICATION NUMBER: US/09/841,730

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: 09/626,896

; PRIOR FILING DATE: 2000-07-27

; PRIOR APPLICATION NUMBER: 09/485,046

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: PCT/US98/15598

; PRIOR FILING DATE: 1998-07-28

; PRIOR APPLICATION NUMBER: 60/054,461

; PRIOR FILING DATE: 1997-08-01

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: FastSeq for windows Version 4.0

; SEQ ID NO 6

; LENGTH: 376

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; US-09-841-730-6

Query Match 80.4%; Score 501; DB 9; Length 376;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRY 60  
|  
Db 268 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 322

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109  
|  
Db 268 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 322

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109  
|  
Db 268 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 322

Db 323 PHTHLVHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIITGKIPAMVVDRCGCS 376

## RESULT 15

US-09-859-211-12  
; Sequence 12, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-jin  
; APPLICANT: McPherson, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/14401  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-859-211-12

Query Match 80.4%; Score 501; DB 9; Length 376;  
Best Local Similarity 80.7%; Pred. No. 4.9e-43;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLDDEHSTESRCRYPPLTVDFEAFGWDWIAPKRYKANYSGECEFNFTVSFWLRY 60  
Db 268 DFGLDDEHSTESRCRYPPLTVDFEAFGWDWIAPKRYKANYSGECEFNFTVSFWLRY 60  
OY 61 PKVSASHL-----EAGPCCPTPTKMSPINMLYFNKGEOIITGKIPAMVVDRCGCS 109  
Db 323 PHTHLVHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIITGKIPAMVVDRCGCS 376

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Job time : 14 secs



Gencore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:02:48 ; Search time 72 Seconds  
(without alignments)  
201.727 Million cell updates/sec

Title: US-09-620-586B-19  
Perfect score: 623  
Sequence: 1 DFGIDCDHESTESRCCRYPL.....KEQIITYGKIPAMVYDRCGCS 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	530.5	85.2	254	22	AAB20152
3	504	80.9	375	20	AAV33845
4	501	80.4	109	22	AAB20141
5	501	80.4	109	23	AAV51935
6	501	80.4	126	15	AAV63161
7	501	80.4	126	19	AAV69883
8	501	80.4	126	20	AAV15386
9	501	80.4	126	22	AAB73182
10	501	80.4	130	22	AAB73189

11	501	80.4	160	22	AAB20153	Growth differentia
12	501	80.4	226	22	AAB73188	Chicken GDF-8. Ga
13	501	80.4	362	22	AAB20132	Turkey growth diff
14	501	80.4	374	23	AAU75623	Chicken promyostat
15	501	80.4	375	15	AAV63160	Human growth diffe
16	501	80.4	375	19	AAV69888	Chicken growth dif
17	501	80.4	375	19	AAV69891	Pig growth differe
18	501	80.4	375	19	AAV69885	Human growth diffe
19	501	80.4	375	19	AAV65460	Human growth diffe
20	501	80.4	375	20	AAV33838	Amino acid sequenc
21	501	80.4	375	20	AAV33839	Amino acid sequenc
22	501	80.4	375	20	AAV33840	Amino acid sequenc
23	501	80.4	375	20	AAV33841	Amino acid sequenc
24	501	80.4	375	20	AAV33843	Amino acid sequenc
25	501	80.4	375	20	AAV33844	Amino acid sequenc
26	501	80.4	375	20	AAV33937	Amino acid sequenc
27	501	80.4	375	20	AAV33938	Amino acid sequenc
28	501	80.4	375	20	AAV33932	Amino acid sequenc
29	501	80.4	375	20	AAV33935	Amino acid sequenc
30	501	80.4	375	20	AAV31189	Human GDF-8 protei
31	501	80.4	375	20	AAV31192	Chicken GDF-8 prote
32	501	80.4	375	20	AAV31194	Turkey GDF-8 prote
33	501	80.4	375	20	AAV97887	Human myostatin.
34	501	80.4	375	21	AAB21087	Human GDF-8. Homo
35	501	80.4	375	21	AAV92035	Human growth diffe
36	501	80.4	375	21	AAV77566	Human growth diffe
37	501	80.4	375	22	AAB73187	Human GDF-8 #2. H
38	501	80.4	375	22	AAB20131	Human growth diffe
39	501	80.4	375	22	AAB20133	Chicken growth dif
40	501	80.4	375	22	AAB20138	Pig growth differe
41	501	80.4	375	23	AAE18659	Human promyostatin
42	501	80.4	375	23	AAE18662	Chicken promyostat
43	501	80.4	375	23	AAE18665	Porcine promyostat
44	501	80.4	375	23	AAE18667	Meleagris gallopav
45	501	80.4	375	23	AAU75620	Human promyostatin

ALIGNMENTS

RESULT 1	
AAB20149	
ID AAB20149	standard; Protein; 109 AA.
XX AC AAB20149;	
XX DT 30-APR-2001	(first entry)
XX DE	Growth differentiation factor 8 AutoVac construct GDF-8 P30-2.
XX KW	Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
KW	T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW	cardiant; human; mutant; mutein.
XX OS	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Clostridium tetani.
OS	Synthetic.
XX FH	
FT FT	Key
FT FT	Location/Qualifiers
FT FT	1..48
FT FT	/note= "identical to residues 267-314 of human
FT FT	GDF-8"
FT FT	Region
FT FT	49..69
FT FT	/note= "tetanus toxoid P2 epitope"
FT FT	Region
FT FT	70..109
FT FT	/note= "identical to residues 336-375 of human
FT FT	GDF-8"
FT FT	Misc-difference 73
FT FT	/note= "Cys-73 may be substituted by Ser to avoid
FT FT	disulfide bond formation"
FT FT	Misc-difference 90..91
FT FT	/note= "optionally replaced by Glu-Gly"
XX	

PN WO200105820-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 20-JUL-2000; 2000WO-DK00413.  
XX  
PR 20-JUL-1999; 99DK-0001014.  
PR 26-JUL-1999; 99US-0145275.  
XX  
PA (MEBI-) M & E BIOTECH AS.  
XX  
PI Halkier T, Mouritsen S, Klysner S;  
XX WPI; 2001-112680/12.  
DR  
XX  
XX  
PT Increasing the muscle mass of animals used in meat production by down  
PT regulating growth differentiation factor 8 (GDF-8) activity in the  
PT animal through induction of anti-GDF-8 antibody production  
XX  
XX  
PS Example 1; Page 101-102; 110pp; English.  
XX  
XX The present sequence is that of AutoVac construct GDF-8 P30-2,  
CC comprising the 109 C-terminal amino acid residues of human  
CC growth differentiation factor 8 (GDF-8) in which residues 49-69 are  
CC replaced by the promiscuous tetanus toxin T-cell epitope P30 (see  
CC AAB20144). It is an object of the invention to produce a  
CC recombinant therapeutic vaccine that is capable of effecting  
CC down-regulation of GDF-8 in order to increase the muscle growth  
CC rate of farm animals. The vaccines (see AAB20145-53) are comprise  
CC of breaking autotolerance against autologous GDF-8. They comprise  
CC the C-terminal portion of human GDF-8 in which a portion of the  
CC native sequence is replaced by a T-cell epitope such as P30, with  
CC minimal disturbance of the authentic 3-dimensional structure of  
CC the protein. Nucleic acids encoding the GDF-8 variants can be used  
CC for genetic immunisation of the animals. Down-regulation of GDF-8  
CC activity can increase muscle mass by up to at least 45% in cattle,  
CC pigs and poultry used for meat production, reducing the need for  
CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to  
CC treat human diseases such as cancer cachexia where muscle atrophy is  
CC pronounced and for patients suffering from acute and chronic heart  
CC failure.  
XX  
SQ Sequence 109 AA;  
Query Match 100.0%; Score 623; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 3.2e-60;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DFGIDCDEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFNNFTVSFWLRV 60  
Db 1 DFGIDCDEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFNNFTVSFWLRV 60  
QY 61 PKVSASHLEAGPCCPTPKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109  
Db 61 PKVSASHLEAGPCCPTPKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109  
RESULT 2  
AAB20152  
ID AAB20152 standard; Protein; 254 AA.  
XX  
AC AAB20152;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Growth differentiation factor 8 AutoVac construct GDF-8 dimer.  
XX  
KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;  
KW T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;  
KW cardiant; human; mutant; mutein.  
XX  
OS Chimeric - Homo sapiens.  
OS Chimeric - Clostridium tetani.

OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Region 1..109  
FT Region /note= "109 C-terminal residues of human GDF-8"  
FT Region 110..124  
FT Region /note= "tetanus toxoid P2 epitope"  
FT Region 125..145  
FT Region /note= "tetanus toxoid P30 epitope"  
FT Region 146..254  
FT /note= "109 C-terminal residues of human GDF-8"  
FT /note= "optionally replaced by Glu-Gly"  
FT /note= "optionally replaced by Glu-Gly"  
FT /note= "optionally replaced by Glu-Gly"  
PN WO200105820-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 20-JUL-2000; 2000WO-DK00413.  
XX  
PR 20-JUL-1999; 99DK-0001014.  
PR 26-JUL-1999; 99US-0145275.  
XX  
PA (MEBI-) M & E BIOTECH AS.  
XX  
PI Halkier T, Mouritsen S, Klysner S;  
XX WPI; 2001-112680/12.  
DR  
XX  
XX  
PT Increasing the muscle mass of animals used in meat production by down  
PT regulating growth differentiation factor 8 (GDF-8) activity in the  
PT animal through induction of anti-GDF-8 antibody production  
XX  
XX  
PS Example 1; Page 105-106; 110pp; English.  
XX  
XX The present sequence is that of AutoVac construct GDF-8 dimer  
CC comprising 2 copies of the 109-amino acid C-terminal region of human  
CC growth differentiation factor 8 (GDF-8, see AAF20141) covalently  
CC connected through the P2 and P30 T-cell epitopes (see AAB20143-44)  
CC of tetanus toxin. It is an object of the invention to produce a  
CC recombinant therapeutic vaccine that is capable of effecting  
CC down-regulation of GDF-8 in order to increase the muscle growth  
CC rate of farm animals. The vaccines (see AAB20145-53) are capable  
CC of breaking autotolerance against autologous GDF-8. They comprise  
CC the C-terminal portion of human GDF-8 in which a portion of the  
CC native sequence is replaced by a T-cell epitope such as P30, with  
CC minimal disturbance of the authentic 3-dimensional structure of  
CC the protein. Nucleic acids encoding the GDF-8 variants can be used  
CC for genetic immunisation of the animals. Down-regulation of GDF-8  
CC activity can increase muscle mass by up to at least 45% in cattle,  
CC pigs and poultry used for meat production, reducing the need for  
CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to  
CC treat human diseases such as cancer cachexia where muscle atrophy is  
CC pronounced and for patients suffering from acute and chronic heart  
CC failure.  
XX  
SQ Sequence 254 AA;  
Query Match 85.2%; Score 530.5; DB 22; Length 254;  
Best Local Similarity 42.9%; Pred. No. 9.9e-50;  
Matches 109; Conservative 0; Mismatches 0; Indels 145; Gaps 2;  
QY 1 DFGIDCDEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCE----- 48  
Db 1 DFGIDCDEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFYLOKYPHTL 60  
QY 49 ----- 48  
Db 61 VHQANPRGSAGPCCPTPKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCSQYIKANSKFIG 120  
QY 49 -----FNNFTVSFWLRVPRKVSASHLE----- 69

Db 121 \* ITELFNNTVSWLRVPKVSASHLEDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAP 180  
QY 70 -----AGPCCTPTKMSPINMLYFNKGEOIIV 95  
Db 181 KRYKANYSCEGCEFFVELQKYPHTHLVHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIIV 240  
QY 96 GKIPIAMVVDRCGS 109  
Db 241 GKIPIAMVVDRCGS 254

RESULT 3  
AAY33845  
ID AAY33845 standard; Protein; 375 AA.  
XX  
AC AAY33845;  
DT 08-DEC-1999 (first entry)  
XX  
DE Amino acid sequence of Ovine Growth Differentiation Factor-8.  
XX  
KW growth differentiation factor; tissue growth; muscle growth;  
KW cell differentiation; animal feed; muscle disorder;  
KW bone degeneration; nerve degeneration; GDF-8; development;  
KW transforming growth factor beta; TGF-beta.  
XX  
OS Ovis aries.  
XX  
PN WO9940181-A1.  
XX  
PD 12-AUG-1999.  
XX  
PF 05-FEB-1999; 99WO-US02511.  
XX  
PR 28-JUL-1998; 98US-0124180.  
PR 05-FEB-1998; 98US-0019070.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Lee S, McPherron AC;  
XX  
DR WPI; 1999-494289/41.  
DR N-PSDB; AA206459.  
XX  
PT New differentiation factor useful for treating neurodegenerative  
PT diseases  
XX  
PS Example 9; Fig 14g; 138pp; English.  
XX  
CC This is the amino acid sequence of the Ovine Growth  
CC Differentiation Factor-8 (GDF-8). Skeletal muscle cDNA libraries from  
CC this species were screened with the murine GDF-8 probe, in order to  
CC isolate the GDF-8. The absolute conservation of the C-terminal region  
CC between species as evolutionary far apart as humans and chickens,  
CC baboons and turkeys, suggests that this region will be highly conserved  
CC in many other species as well.  
CC GDF-8 has been shown to result in increased bone and muscle mass (such  
CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic  
CC animals and forms of animal feed that can inhibit/reduce production of  
CC GDF-8 are of commercial interest.  
CC GDF-8 expression may also have a role in the therapy of abnormal growth  
CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8  
CC antisense molecule or dominant negative polypeptide could be used with  
CC foetal or adult muscle cells, bone cells or progenitor cells. These  
CC agents can be administered to a patient suffering from a disorder such  
CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,  
CC osteoporosis, bone degenerative diseases, obesity or other adipocyte  
CC cell disorders, and aging for example.  
XX  
SQ Sequence 375 AA;

Query Match 80.9%; Score 504; DB 20; Length 375;

Best Local Similarity 79.5%; Pred. No. 1.2e-46;  
Matches 93; Conservative 2; Mismatches 6; Indels 16; Gaps 2;  
QY 1 DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGCEFFNFTVSWLRV 60  
Db 267 DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGCEFF-----LFL 318  
QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGEOIIVGKIPIAMVVDRCGS 109  
Db 319 QKYPHTHLVHQANPKGSAGPCCPTPTKMSPINMLYFNKGEOIIVGKIPIAMVVDRCGS 375

RESULT 4  
AAB20141  
ID AAB20141 standard; Protein; 109 AA.  
XX  
AC AAB20141;  
DT 30-APR-2001 (first entry)  
XX  
DE Human growth differentiation factor 8 C-terminal region.  
XX  
KW Growth differentiation factor 8; GDF-8; myostatin; down-regulation;  
KW vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200105820-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 20-JUL-2000; 2000WO-DK00413.  
XX  
PR 20-JUL-1999; 99DK-0001014.  
PR 26-JUL-1999; 99US-0145275.  
XX  
PA (MEBI-) M & E BIOTECH AS.  
XX  
PI Halkier T, Mouritsen S, Klysner S;  
XX  
DR WPI; 2001-112680/12.  
XX  
PT Increasing the muscle mass of animals used in meat production by down  
PT regulating growth differentiation factor 8 (GDF-8) activity in the  
PT animal through induction of anti-GDF-8 antibody production  
XX  
PS Claim 17; Page 93-94; 110pp; English.  
XX  
CC The present sequence comprises the 109 amino acid residue  
CC C-terminal region of human growth differentiation factor 8  
CC (GDF-8), i.e. residues 267-375 of the full-length protein (see  
CC AAB20131). The homodimer of this region is thought to be the  
CC biologically active form of GDF-8. It is an object of the  
CC invention to produce a recombinant therapeutic vaccine capable of  
CC effecting down-regulation of GDF-8 in order to increase the muscle  
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)  
CC are provided that are capable of breaking autotolerance against  
CC autologous GDF-8. These comprise the C-terminal portion of human  
CC GDF-8 in which a portion of the native sequence is replaced by a  
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope  
CC p2 or p30. The high number (9) of Cys residues in the C-terminal  
CC region limits the possible sites in which the T-cell epitope can be  
CC positioned without major disturbance of the native 3-dimensional  
CC structure of the protein. Nucleic acids encoding the GDF-8 variants  
CC can be used for genetic immunisation of the animals. Down-regulation  
CC of GDF-8 activity can increase muscle mass by up to at least 45% in  
CC cattle, pigs and poultry used for meat production, reducing the need  
CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to  
CC treat human diseases such as cancer cachexia where muscle atrophy is  
CC pronounced and for patients suffering from acute and chronic heart  
CC failure.  
XX

SQ	Sequence	109 AA;	
Query Match			
Best Local Similarity		80.4%;	Score 501; DB 22; Length 109;
Matches		92; Conservative	1; Mismatches 11; Indels 10; Gaps 2;
QY	1	DFGLDCDEHSTESRCRYP	LTVDFEAFGWDWIAPKRYKANYCSGECEFNFTVSWLRV 60
Db	1	DFGLDCDEHSTESRCRYP	LTVDFEAFGWDWIAPKRYKANYCSGECEF-----VFLQKY 55
QY	61	PKVSASHL----	EAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db	56	PHTHLVHQANPRGSAGP	CCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
RESULT 5			
AAM51935			
ID	AAM51935 standard; protein; 109 AA.		
XX			
AC	AAM51935;		
XX			
DT	01-FEB-2002 (first entry)		
XX			
DE	Human TGFbeta protein superfamily protein GDF8.		
XX			
KW	Human; TGFbeta; transforming growth factor beta; mutant; antagonist;		
KW	agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;		
KW	formation; fibrosis; cirrhosis; osteopathic; antipsoriatic;		
KW	antifibrotic; hepatotropic; vulnerary; GDF8.		
XX			
OS	Homo sapiens.		
XX			
PN	DE10026713-A1.		
XX			
PD	06-DEC-2001.		
XX			
PF	30-MAY-2000; 2000DE-1026713.		
XX			
PR	30-MAY-2000; 2000DE-1026713.		
XX			
PA	(SEBA/) SEBALD W.		
XX			
PI	Sebald W, Nickel J;		
XX			
DR	WPI; 2002-042559/06.		
XX			
PT	New mutein of transforming growth factor-beta superfamily protein,		
PT	useful for treating or preventing e.g. ectopic bone formation, competes		
PT	for receptor binding		
XX			
PS	Disclosure; Fig 6; 54pp; German.		
XX			
CC	The present invention relates to muteins of a chain of a protein which,		
CC	when in the form of a homodimer, has antagonistic or partial agonistic		
CC	activity, and where the mutation results in the protein binding with low		
CC	affinity to its receptor. The protein is a member of the transforming		
CC	growth factor beta (TGFbeta) superfamily. The mutant sequences of the		
CC	invention can be used in the treatment of diseases associated with the		
CC	overexpression of TGFbeta family proteins, including ectopic bone		
CC	formation, psoriasis, muscular atrophy, scar formation, fibrosis and		
CC	cirrhosis. The present sequence is the human GDF8 protein.		
XX			
SQ	Sequence	109 AA;	
Query Match			
Best Local Similarity		80.4%;	Score 501; DB 23; Length 109;
Matches		92; Conservative	1; Mismatches 11; Indels 10; Gaps 2;
QY	1	DFGLDCDEHSTESRCRYP	LTVDFEAFGWDWIAPKRYKANYCSGECEFNFTVSWLRV 60
Db	1	DFGLDCDEHSTESRCRYP	LTVDFEAFGWDWIAPKRYKANYCSGECEF-----VFLQKY 55
QY	61	PKVSASHL----	EAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db	61	PKVSASHL----	EAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109

Db	56	PHTHLVHQANPRGSAGP	CCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
RESULT 6			
AAR63161			
ID	AAR63161 standard; Protein; 126 AA.		
XX			
AC	AAR63161;		
XX			
DT	23-JUN-1995 (first entry)		
XX			
DE	Mouse growth differentiation factor-8 partial sequence.		
XX			
KW	Growth differentiation factor-8; GDF-8; cell proliferation;		
KW	adipocyte; obesity; transforming growth factor-beta.		
XX			
OS	Mus musculus.		
XX			
PN	WO9421681-A.		
XX			
PD	29-SEP-1994.		
XX			
PF	18-MAR-1994; 94WO-US03019.		
XX			
PR	19-MAR-1993; 93US-0033923.		
XX			
PA	(UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.		
XX			
PI	Lee S, Mcpherron AC;		
XX			
DR	WPI; 1994-316943/39.		
DR	Q-PSDB; Q76380.		
XX			
PT	New growth differentiation factor 8 - useful for treatment and		
PT	diagnosis of cell proliferative disorders esp. of muscle.		
XX			
PS	Disclosure; Page 41; 84pp; English.		
XX			
CC	GDF-8 can be used to maintain cells before transplantation; to		
CC	improve efficiency of cell fusion and to treat obesity or diseases		
CC	related to abnormal adipocyte proliferation.		
XX			
SQ	Sequence	126 AA;	
Query Match			
Best Local Similarity		80.4%;	Score 501; DB 15; Length 126;
Matches		92; Conservative	1; Mismatches 11; Indels 10; Gaps 2;
QY	1	DFGLDCDEHSTESRCRYP	LTVDFEAFGWDWIAPKRYKANYCSGECEFNFTVSWLRV 60
Db	18	DFGLDCDEHSTESRCRYP	LTVDFEAFGWDWIAPKRYKANYCSGECEF-----VFLQKY 72
QY	61	PKVSASHL----	EAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db	73	PHTHLVHQANPRGSAGP	CCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
RESULT 7			
AAW69883			
ID	AAW69883 standard; Protein; 126 AA.		
XX			
AC	AAW69883;		
XX			
DT	07-DEC-1998 (first entry)		
XX			
DE	Murine growth differentiation factor-8 C-terminal fragment.		
XX			
KW	Growth differentiation factor-8; GDF-8; mouse; transgenic animal;		
KW	transforming growth factor-beta; muscle; meat; inhibitor; obesity;		
KW	neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;		
XX	therapy.		



OS Mus .ap. Location/Qualifiers  
XX Key 13..14  
FH Cleavage-site 16..17  
FT Cleavage-site 17..126  
FT Protein /note= "mature polypeptide"  
XX WO9833887-A1.  
XX PD 06-AUG-1998.  
XX PF 05-FEB-1998; 98WO-US02479.  
XX PR 23-MAY-1997; 97US-0862445.  
PR 05-FEB-1997; 97US-0795071.  
PR 28-APR-1997; 97US-0847910.  
XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX PI Lee S, McPherron AC;  
XX DR WPI: 1998-437444/37.  
DR N-PSDB; AAV45809.  
XX PT Transgenic animals with gene for growth differentiation factor-8  
PT disrupted - have increased muscle and reduced cholesterol contents,  
PT also use of GDF-8 inhibitors for treating cancer, obesity,  
PT neuromuscular disease  
XX PS Example 2; Page 58; 125pp; English.  
XX CC This is the amino acid sequence of the C-terminal portion of mouse  
CC growth differentiation factor-8 (GDF-8), a novel member of the  
CC transforming growth factor-beta superfamily that appears to relate  
CC to various cell proliferative disorders, especially those involving  
CC muscle, nerve and adipose tissue. The sequence was deduced from a  
CC partial genomic clone (see AAV45809). A full-length sequence (see  
CC AAW30689) has been deduced from a cDNA clone (see AAV42113). The  
CC invention provides novel mammalian and avian GDF-8 proteins (see  
CC AAW69883-92). A transgenic non-human animal is claimed in which  
CC GDF-8 expression is disrupted or interfered with. Also claimed  
CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb  
CC from these animals; (2) method for increasing muscle mass in  
CC animals by administering an antibody (Ab) that binds to GDF-8; (3)  
CC inhibiting the action of GDF-8 by treating foetal or adult muscle  
CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic  
CC acid encoding a GDF-8 protein truncated by loss of the C-terminal  
CC active fragment. The transgenic animals have increased muscle mass  
CC and for poultry reduced cholesterol contents. Method (3) is used  
CC to treat muscle wasting or neuromuscular diseases, muscular atrophy  
CC and aging, particularly muscular dystrophy, spinal cord or  
CC traumatic injuries, congestive or obstructive lung disease, AIDS  
CC and cachexia. Method (4) is used to treat cancer of muscle,  
CC connective tissue and bone, or obesity. Also (not claimed) GDF-8  
CC can be used to maintain myoblasts intended for transplanting or to  
CC improve efficiency of fusion. Ab can be used to detect and  
CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),  
CC also for immunotherapy and in vivo imaging.  
XX SQ Sequence 126 AA;  
Query Match 80.4%; Score 501; DB 19; Length 126;  
Best Local Similarity 80.7%; Pred. No. 7.3e-47;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60  
DB 18 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRV 72  
OY 61 PKVSASHL-----EAGPCCFTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 109  
DB 73 PHTHLVHOANRGSAGPCCFTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 126

RESULT 8  
ID AAY15386 standard; Protein; 126 AA.  
XX AAY15386;  
XX AC AAY15386;  
XX DT 08-DEC-1999 (first entry)  
XX DE C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).  
XX growth differentiation factor; tissue growth; muscle growth;  
KW cell differentiation; animal feed; muscle disorder;  
KW bone degeneration; nerve degeneration; GDF-8; development;  
KW transforming growth factor beta; TGF-beta.  
XX OS Mus musculus.  
XX FH Key Location/Qualifiers  
FH Cleavage-site 13..14  
FT Cleavage-site /label= Potential\_proteolytic\_cleavage\_site  
FT Cleavage-site 16..17  
FT /label= Potential\_proteolytic\_cleavage\_site  
FT /note= "cleavage generates mature protein"  
XX PN WO9940181-A1.  
XX PD 12-AUG-1999.  
XX PF 05-FEB-1999; 99WO-US02511.  
XX PR 28-JUL-1998; 98US-0124180.  
PR 05-FEB-1998; 98US-0019070.  
XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE;  
XX PI Lee S, McPherron AC;  
XX DR WPI: 1999-494289/41.  
DR N-PSDB; AAZ06446.  
XX PT New differentiation factor useful for treating neurodegenerative  
PT diseases  
XX PS Example 2; Fig 2a; 138pp; English.  
XX CC This is the amino acid sequence of the C-terminal region of the GDF-8  
CC precursor protein. The predicted GDF-8 sequence contains two potential  
CC proteolytic processing sites.  
CC Cleavage of the precursor at the second of these sites would generate  
CC a mature C terminal fragment 109 amino acids in length with a predicted  
CC molecular weight of 12,400.  
CC GDF-8 has been shown to result in increased bone and muscle mass (such  
CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic  
CC animals and forms of animal feed that can inhibit/reduce production of  
CC GDF-8 are of commercial interest.  
CC GDF-8 expression may also have a role in the therapy of abnormal growth  
CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8  
CC antisense molecule or dominant negative polypeptide could be used with  
CC foetal or adult muscle cells, bone cells or progenitor cells. These  
CC agents can be administered to a patient suffering from a disorder such  
CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,  
CC osteoporosis, bone degenerative diseases, obesity or other adipocyte  
CC cell disorders, and aging for example.  
XX SQ Sequence 126 AA;  
Query Match 80.4%; Score 501; DB 20; Length 126;  
Best Local Similarity 80.7%; Pred. No. 7.3e-47;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRV 60

```
Db      18 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 72
QY      61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db      73 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 126

RESULT 9
AAB73182
ID      AAB73182 standard; Protein; 126 AA.
AC      AAB73182;
XX      11-MAY-2001 (first entry)
DE      Murine GDF-8 #1.
XX      Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW      neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW      muscular dystrophy; musculodegenerative disease; tissue repair;
KW      muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW      traumatic injury; congestive obstructive pulmonary disease.
XX      Mus sp.
XX      WO200112777-A2.
XX      22-FEB-2001.
XX      17-AUG-2000; 2000WO-US22884.
XX      19-AUG-1999; 99US-0378238.
XX      (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX      Lee S, McPherron AC;
XX      WPI; 2001-211209/21.
XX      N-PSDB; AAF63547.
XX      New substantially purified growth differentiation factor-8 polypeptide,
PT      useful for treating muscle wasting disease, obesity, muscular
PT      dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT      and cachexia
XX      Example 2; Fig 2; 124pp; English.
XX      The present invention relates to growth differentiation factor-8 (GDF-8)
CC      coding sequences and proteins. The present sequence is a GDF-8 protein,
CC      which was isolated in the present invention. GDF-8 is useful for treating
CC      neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC      muscular dystrophy), musculodegenerative diseases or in tissue repair due
CC      to trauma, obesity and disorders related to abnormal proliferation of
CC      adipocytes. GDF-8 is also useful for treating malignancies of the various
CC      organ systems, particularly cells in muscle or adipose tissues and in
CC      gene therapy for the treatment of cell proliferative or immunological
CC      diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC      treating muscle wasting disease, neuromuscular disorder, spinal cord
CC      injury, traumatic injury, congestive obstructive pulmonary disease
CC      (COPD), AIDS or cachexia.
XX      Sequence 126 AA;

Query Match      80.4%; Score 501; DB 22; Length 126;
Best Local Similarity 80.7%; Pred. No. 7.3e-47;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY      1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSEWLRV 60
Db      18 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 72
QY      61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db      77 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 130

Db      73 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
RESULT 10
AAB73189
ID      AAB73189 standard; Protein; 130 AA.
AC      AAB73189;
XX      11-MAY-2001 (first entry)
DE      Rat GDF-8.
XX      Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW      neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW      muscular dystrophy; musculodegenerative disease; tissue repair;
KW      muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW      traumatic injury; congestive obstructive pulmonary disease.
XX      Rattus sp.
XX      WO200112777-A2.
XX      22-FEB-2001.
XX      17-AUG-2000; 2000WO-US22884.
XX      19-AUG-1999; 99US-0378238.
XX      (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX      Lee S, McPherron AC;
XX      WPI; 2001-211209/21.
XX      N-PSDB; AAF63555.
XX      New substantially purified growth differentiation factor-8 polypeptide,
PT      useful for treating muscle wasting disease, obesity, muscular
PT      dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT      and cachexia
XX      Example 9; Fig 2; 124pp; English.
XX      The present invention relates to growth differentiation factor-8 (GDF-8)
CC      coding sequences and proteins. The present sequence is a GDF-8 protein,
CC      which was isolated in the present invention. GDF-8 is useful for treating
CC      neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC      muscular dystrophy), musculodegenerative diseases or in tissue repair due
CC      to trauma, obesity and disorders related to abnormal proliferation of
CC      adipocytes. GDF-8 is also useful for treating malignancies of the various
CC      organ systems, particularly cells in muscle or adipose tissues and in
CC      gene therapy for the treatment of cell proliferative or immunological
CC      diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC      treating muscle wasting disease, neuromuscular disorder, spinal cord
CC      injury, traumatic injury, congestive obstructive pulmonary disease
CC      (COPD), AIDS or cachexia.
XX      Sequence 130 AA;

Query Match      80.4%; Score 501; DB 22; Length 130;
Best Local Similarity 80.7%; Pred. No. 7.5e-47;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY      1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSEWLRV 60
Db      22 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 76
QY      61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db      77 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 130
```

ID	AA	Protein	Length
RESULT 11*			
AAB20153	standard	Protein; 160 AA.	
XX			
AC	AAB20153;		
XX			
DT	30-APR-2001	(first entry)	
XX			
DE		Growth differentiation factor 8 AutoVac construct GDF-8 ext.	
XX			
KW		Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin; T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.	
KW			
XX			
OS	Chimeric - Homo sapiens.		
OS	Chimeric - Clostridium tetani.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	1..15	
FT		/note= "identical to residues 215-230 of human GDF-8"	
FT	Region	16..36	
FT		/note= "tetanus toxoid P30 epitope"	
FT	Region	37..51	
FT		/note= "tetanus toxoid P2 epitope"	
FT	Region	52..160	
FT		/note= "identical to residues 267-375 of human GDF-8"	
FT	Misc-difference 124		
FT		/note= "Cys-124 may be substituted by Ser to avoid disulfide bond formation"	
FT	Misc-difference 141..142		
FT		/note= "optionally replaced by Glu-Gly"	
PN	WO200105820-A2.		
XX			
PD	25-JAN-2001.		
XX			
PF	20-JUL-2000; 2000WO-DK00413.		
XX			
PR	20-JUL-1999; 99DK-0001014.		
PR	26-JUL-1999; 99US-0145275.		
XX			
PA	(MEBI-) M & E BIOTECH AS.		
PI	Halkier T, Mouritsen S, Klysner S;		
DR	WPI; 2001-112680/12.		
XX			
XX			
PT			
PT			
PT			
PT			
XX			
PS			
XX			

Example 1; Page 107-108; 110pp; English.

The present sequence is that of AutoVac construct GDF-8 ext, which consists of the C-terminal 160 amino acids of human growth differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36 substituted by the promiscuous tetanus toxin T-cell epitope P30 (see AAB20144) and residues 37-51 substituted by tetanus toxin T-cell epitope P2 (see AAB20143). It is an object of the invention to produce a recombinant therapeutic vaccine that is capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. The vaccines (see AAB20145-53) are capable of breaking autotolerance against autologous GDF-8. They comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as P30, with minimal disturbance of the authentic 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for

CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to  
CC treat human diseases such as cancer cachexia where muscle atrophy is  
CC pronounced and for patients suffering from acute and chronic heart  
CC failure.

XX

SQ Sequence 160 AA;

Query Match 80.4%; Score 501; DB 22; length 160;  
Best Local Similarity 80.7%; Pred. No. 9.5e-47;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCCRPLVDFEAFGWDWIAPKRYKANYSGECEFNFTVSFWLRV 60  
|||||  
Db 52 DFGLDCEHSTESRCCRPLVDFEAFGWDWIIAPKRYKANYSGECEF----VFLoKy 106  
|||||

QY 61 PKVASSHL-----EAGPCCTPTKMSPINMLLYENGKEQLIYGKIPAMVVDRCGCS 109  
|-|||  
Db 107 PHTLVHQANPRGSAGPCCCTPTKMSPINMLLYENGKEQLIYGKIPAMVVDRCGCS 160  
|||||

```

RESULT 12
AAB73188
ID AAB73188 standard; Protein; 226 AA.
XX
AC AAB73188;
XX
DT 11-MAY-2001 (first entry)
XX
DE Chicken GDF-8.
XX
KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musculodegenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.
XX
OS Gallus gallus.
XX
PN WO200112777-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22884.
XX
PR 19-AUG-1999; 99US-0378238.
XX
PI (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, McPherron AC;
XX
DR WPI; 2001-211209/21.
DR N-PSDB; AAF63554.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -
XX
XX
PS Example 9; Fig 2; 124pp; English.
XX
XX
The present invention relates to growth differentiation factor-8 (GDF-8)
coding sequences and proteins. The present sequence is a GDF-8 protein,
which was isolated in the present invention. GDF-8 is useful for treating
neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
muscular dystrophy), musculodegenerative diseases or in tissue repair due
to trauma, obesity and disorders related to abnormal proliferation of
adipocytes. GDF-8 is also useful for treating malignancies of the various
organ systems, particularly cells in muscle or adipose tissues and in
gene therapy for the treatment of cell proliferative or immunological
diseases mediated by GDF-8. In addition, GDF-8 is also useful for
treating muscle wasting disease, neuromuscular disorder, spinal cord
injury, traumatic injury, congestive obstructive pulmonary disease
(COPD), AIDS or cachexia.

```



XX Sequence 226 AA;

Query Match 80.4%; Score 501; DB 22; Length 226;  
Best Local Similarity 80.7%; Pred. No. 1.4e-46;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGFNNFTVSFWLRY 60  
118 DFGLCDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGF-----VFLQKY 172

OY 61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 109  
173 PHTHLVHQANPRGSAGPCCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 226

RESULT 13

AAB20132  
ID AAB20132 standard; Protein; 362 AA.

AC AAB20132;

DT 30-APR-2001 (first entry)

DE Turkey growth differentiation factor 8.

KW Growth differentiation factor 8; GDF-8; myostatin; down-regulation;

KM vaccine; muscle; meat; cachexia; cardiant; turkey.

OS Meleagris gallopavo.

PN WO200105820-A2.

PD 25-JAN-2001.

PF 20-JUL-2000; 2000WO-DK00413.

PR 20-JUL-1999; 99DK-0001014.

PR 26-JUL-1999; 99US-0145275.

PA (MEBI-) M & E BIOTECH AS.

PI Halkier T, Mouritsen S, Klysner S;

DR WPI; 2001-112680/12.

PT Increasing the muscle mass of animals used in meat production by down

PT regulating growth differentiation factor 8 (GDF-8) activity in the

PS animal through induction of anti-GDF-8 antibody production -

XX Example 1; Page 76-78; 110pp; English.

CC The present sequence is that of turkey growth differentiation factor

CC 8 (GDF-8), also called myostatin. It is an object of the invention

CC to produce a recombinant therapeutic vaccine capable of effecting

CC down-regulation of GDF-8 in order to increase the muscle growth

CC rate of farm animals. Variants of GDF-8 (see AAB20145-53) are

CC provided that are capable of breaking autotolerance against

CC autologous GDF-8. These comprise a C-terminal portion of human

CC GDF-8 in which a portion of the native sequence is replaced by a

CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope

CC p2 or p30. Nucleic acids encoding the GDF-8 variants can be used

CC for genetic immunisation of the animals. Down-regulation of GDF-8

CC activity is used to increase muscle mass by up to at least 45%

CC in cattle, pigs and poultry used for meat production, reducing the

CC need for antibiotic feed-additives. Anti-GDF8 vaccines can be used

CC to treat human diseases such as cancer cachexia where muscle atrophy

Best Local Similarity 80.7%; Pred. No. 2.4e-46;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGFNNFTVSFWLRY 60  
Db 254 DFGLCDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGF-----VFLQKY 308

OY 61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 109  
Db 309 PHTHLVHQANPRGSAGPCCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 362

RESULT 14

AAU75623  
ID AAU75623 standard; Protein; 374 AA.

AC AAU75623;

DT 21-MAY-2002 (first entry)

DE Chicken promyostatin.

KW Chicken; promyostatin; immunomodulator; antidepressant; anorectic;

KM neuroprotective; antidiabetic; growth differentiation factor receptor;

KM myostatin receptor; GDF; muscle tissue; adipose tissue; cachexia;

KW wasting disorder; anorexia; muscular dystrophy; neuromuscular disease;

OS Gallus gallus.

PN WO200210214-A2.

PD 07-FEB-2002.

PF 26-JUL-2001; 2001WO-US23615.

PR 27-JUL-2000; 2000US-0626896.

PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

DR WPI; 2002-217116/27.

DR N-PSDB; ABK15396.

PT New growth differentiation factor (GDF) receptors and modulators,

PT useful for ameliorating wasting disorders such as cachexia, muscular

PT dystrophy or neuromuscular disease or a metabolic disorder such as

PT obesity or type II diabetes -

XX Claim 22; Fig 1; 184pp; English.

CC The invention relates to a substantially purified growth differentiation

CC factor (GDF) receptor, specifically a myostatin receptor, or its

CC functional peptide portion. Also described is a method of modulating an

CC effect of myostatin on a cell by contacting the cell with an agent that

CC affects myostatin signal transduction in the cell. The method and the

CC receptor are useful for ameliorating the severity of a pathological

CC condition characterised by an abnormal amount, development or metabolic

CC activity of muscle or adipose tissue in a subject, particularly a wasting

CC disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular

CC disease) or a metabolic disorder (e.g. obesity or type II diabetes). The

CC present sequence represents the amino acid sequence of chicken

CC promyostatin.

XX Sequence 374 AA;

Query Match 80.4%; Score 501; DB 23; Length 374;

Best Local Similarity 80.7%; Pred. No. 2.5e-46;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGFNNFTVSFWLRY 60

118 DFGLCDDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYSCEGF-----VFLQKY 308





3. 1. 2.

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1.

GenCore version 5.1.4\_P5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2003, 15:08:53 ; Search time 33 Seconds  
(without alignments)  
680.580 Million cell updates/sec

Title: US-09-620-586B-19

Perfect score: 623

Sequence: 1 DRGLDCDEHSTESRCRYPD.....KEQIYGRIPAMVVDRCGS 109

Scoring table: BLOSUM62

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTRMBL\_21:\*
- 2: sp\_archaea:\*
- 3: sp\_bacteria:\*
- 4: sp\_fungi:\*
- 5: sp\_human:\*
- 6: sp\_invertebrate:\*
- 7: sp\_mammal:\*
- 8: sp\_mhc:\*
- 9: sp\_organelle:\*
- 10: sp\_phage:\*
- 11: sp\_plant:\*
- 12: sp\_rodent:\*
- 13: sp\_virus:\*
- 14: sp\_vertebrate:\*
- 15: sp\_unclassified:\*
- 16: sp\_rvivirus:\*
- 17: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	501	80.4	162	6	Q9TSY2	Q9tsy2 sus scrofa
2	501	80.4	375	6	Q9GM97	Q9gm97 equus caball
3	501	80.4	375	6	Q95J86	Q95j86 macaca fasc
4	501	80.4	375	13	Q8UWD8	Q8uwd8 columba liv
5	501	80.4	375	13	Q8UWD7	Q8uwd7 coturnix ch
6	500	80.3	375	13	Q98SP0	Q98sp0 gallus gall
7	495	79.5	375	13	Q8UWD9	Q8uwd9 anser anser
8	493	79.1	375	13	Q8UWE0	Q8uwe0 anas platyr
9	490	78.7	375	6	Q8WNS6	Q8wns6 bos taurus
10	487	78.2	185	6	Q95N11	Q95n11 capra hircu
11	480	77.0	185	6	Q9MZ18	Q9mz18 ovis aries
12	465	74.6	389	13	Q90YY0	Q90yy0 ictalurus p
13	464	74.5	385	13	Q90W05	Q90w05 sparus aura
14	463	74.3	373	13	Q9DDI8	Q9ddi8 salmo salar
15	463	74.3	373	13	Q90ZD2	Q90zd2 oncorhynch
16	463	74.3	373	13	Q90ZD1	Q90zd1 oncorhynch

17	463	74.3	376	13	Q98TB4	Q98tb4 oreochromis
18	463	74.3	376	13	Q90WC9	Q90wc9 morone saxa
19	463	74.3	376	13	Q90WC8	Q90wc8 morone amer
20	463	74.3	376	13	Q90W06	Q90w06 umbrina cir
21	462	74.2	373	13	Q90W17	Q90w17 salmo salar
22	458	73.5	377	13	Q98TB3	Q98tb3 morone chry
23	456	73.2	373	13	Q98UB3	Q98ub3 salvelinus
24	447	71.7	359	13	Q8QG53	Q8qg53 sparus aura
25	426	68.4	96	13	Q9W759	Q9w759 calrina mos
26	415	66.6	107	6	Q9BG54	Q9bg54 sus scrofa
27	293	47.0	78	6	Q9XS86	Q9xs86 equus caball
28	286	45.9	58	6	Q95MF3	Q95mf3 sus scrofa
29	262	42.1	191	13	Q98TY4	Q98ty4 perca flave
30	257	41.3	104	13	Q90Z79	Q90z79 ictalurus p
31	255	40.9	263	13	Q8QH11	Q8qh11 umbrina cir
32	253.5	40.7	598	5	Q9XZ62	Q9xz62 drosophila
33	253.5	40.7	598	5	Q9V4F4	Q9v4f4 drosophila
34	230	36.9	370	13	Q91350	Q91350 xenopus lae
35	225.5	36.2	349	5	Q97138	Q97138 brugia mala
36	221	35.5	395	13	Q9PWG6	Q9pwg6 anguilla ja
37	217.5	34.9	392	13	Q9PWR8	Q9pwr8 carassius a
38	217.5	34.9	393	13	Q90261	Q90261 brachydanio
39	215.5	34.6	115	13	Q9DGF1	Q9dgf1 cyprinus ca
40	215.5	34.6	115	13	Q9DGF6	Q9dge6 oryzias lat
41	215.5	34.6	426	4	Q9HBP0	Q9hbp0 homo sapien
42	214.5	34.4	115	13	Q9DGE9	Q9dge9 cyprinus ca
43	214.5	34.4	119	6	Q95KPI	Q95kpi ailurus ful
44	214.5	34.4	367	13	Q91696	Q91696 xenopus lae
45	214.5	34.4	424	13	Q98SP9	Q98sp9 meleagris g

ALIGNMENTS

Q9TSY2	Q9TSY2	PRELIMINARY;	PRT;	162 AA.
AC	Q9TSY2;			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	Myostatin (Fragment).			
GN	MSTN.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20078370; PubMed=10612246;			
RA	Stratil A., Kopecky M.;			
RT	"Genomic organization, sequence and polymorphism of the porcine			
RT	myostatin (GDF8; MSTN) gene."			
RL	Anim. Genet. 30:468-470(1999).			
CC	-I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	EMBL; AJ237920; CAB40844.1; -.			
DR	HSSP; P18075; 1BMP.			
DR	InterPro; IPR002400; GF_cysknot.			
DR	InterPro; IPR001639; TGFb_N.			
DR	InterPro; IPR001111; TGFb_N.			
DR	Pfam; PF00019; TGF-beta; 1.			
DR	Pfam; PF00688; TGFb_propeptide; 1.			
DR	PRINTS; PR00438; GFCYSKNOT.			
DR	ProDom; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFb; 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
KW	Glycoprotein.			
FT	NON_TER			
SO	SEQUENCE	162 AA;	18290 MW;	FE3535334512856E CRC64;
Query Match				
Best Local Similarity 80.4%; Score 501; DB 6; Length 162;				
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;				

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QY      1  DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANCYSGCECFNNFTVSFWLRV 60
      |||||||
Db      54  DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANCYSGCECF-----VFLQKY 108

QY      61  PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGEQIITYGKIPAMVVDRCGCS 109
      |
Db      109 PHTHLVHOANPRGSAGPCCPTPTKMSPINMLYFNKGEQIITYGKIPAMVVDRCGCS 162

RESULT 2
O9GM97
ID      O9GM97      PRELIMINARY;      PRT;      375 AA.
AC      O9GM97;
DT      01-MAR-2001 (TREMBlrel. 16, Created)
DT      01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE      Myostatin.
GN      MSTN.
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX      NCBI_TaxID=9796;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=THROUGHBRED;
RA      Hosoyama T., Yamanouchi K., Tojo H., Tachi C.;
RT      "Molecular cloning of equine myostatin cDNA and serum level of
RT      myostatin in horse.";
RL      Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR      EMBL; AB033541; BAB16046.1; -.
DR      HSSP; P18075; 1BMP.
DR      InterPro; IPR002048; EF-hand.
DR      InterPro; IPR001839; TGFb.
DR      InterPro; IPR001111; TGFb_N.
DR      Pfam; PF00019; TGF-beta; 1.
DR      Pfam; PF00688; TGFb_propeptide; 1.
DR      ProDom; PD000357; TGFb; 1.
DR      SMART; SM00204; TGFb; 1.
DR      PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR      PROSITE; PS00250; TGF_BETA_1; 1.
KW      Glycoprotein.
SQ      SEQUENCE 375 AA; 42736 MW; 6F424ECBEE4D9936 CRC64;

Query Match      80.4%; Score 501; DB 6; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY      1  DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANCYSGCECFNNFTVSFWLRV 60
      |||||||
Db      267  DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANCYSGCECF-----VFLQKY 321

QY      61  PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGEQIITYGKIPAMVVDRCGCS 109
      |
Db      322 PHTHLVHOANPRGSAGPCCPTPTKMSPINMLYFNKGEQIITYGKIPAMVVDRCGCS 375

RESULT 3
O95J86
ID      O95J86      PRELIMINARY;      PRT;      375 AA.
AC      O95J86;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE      Myostatin.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC      Cercopitheciinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A.

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RC TISSUE-GASTROCNEMITUS;
RA Smock S.L., Owen T.A.;
RT "Cloning of the open reading frame DNA for macaque fascicularis
RL (cynomolgus macaque) myostatin (GDF8).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL AY057570; AAL17640.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42722 MW; 2149B46AC7D446E7 CRC64;

Query Match      80.4%; Score 501; DB 6; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCCRYPPLTVDFEAFGMDWIIAPKRYKANYSCEGEFNNFTVSFWLRV 60
   |||||||
Db 267 DFGLDCEHSTESRCCRYPPLTVDFEAFGMDWIIAPKRYKANYSCEGEF---VFLOKY 321

QY 61 PKVASASHL-----EAGPCCTPTKMSPINMLYFNKGEOIYGKIPAMVVDRCGCS 109
   |
Db 322 PHTHLVHQANPRGSAGPCCPTPKMSPINMLYFNKGEOIYGKIPAMVVDRCGCS 375

RESULT 4
Q8UWD8 PRELIMINARY; PRT; 375 AA.
AC Q8UWD8;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL AF440863; AAL35277.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42739 MW; 88296F0AE779476E CRC64;

Query Match      80.4%; Score 501; DB 13; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCCRYPPLTVDFEAFGMDWIIAPKRYKANYSCEGEFNNFTVSFWLRV 60
   |||||||
Db 267 DFGLDCEHSTESRCCRYPPLTVDFEAFGMDWIIAPKRYKANYSCEGEF---VFLOKY 321

QY 61 PKVASASHL-----EAGPCCTPTKMSPINMLYFNKGEOIYGKIPAMVVDRCGCS 109
   |
Db 322 PHTHLVHQANPRGSAGPCCPTPKMSPINMLYFNKGEOIYGKIPAMVVDRCGCS 375

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RESULT 5
Q8UWD7 PRELIMINARY; PRT; 375 AA.
AC Q8UWD7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Coturnix chinensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=46218;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440864; AAL35278.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb_N.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42721 MW; B893B1IA42DE0725 CRC64;

Query Match
Best Local Similarity 80.4%; Score 501; DB 13; Length 375;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIAPKRYKANYCSGECENFTVSFWLRV 60
DB 267 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIAPKRYKANYCSGECENFTVSFWLRV 60
QY 61 PKVSASHL-----EAGPCTPTKMSPIINMLYFNKGKEQIITGKIPAMVVDRCGCS 109
DB 322 PHTHLVHQANPRGSAGPCCPTPKMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 375

RESULT 6
Q8USP0 PRELIMINARY; PRT; 375 AA.
AC Q8USP0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Yang W., Zhu D.;
RT "Genomic structure and expression of the chicken GDF-8 during
RT development."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF346599; AAK18000.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR InterPro; IPR001111; TGFb_N.
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DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42717 MW; D980E286426E4DAF CRC64;

Query Match
Best Local Similarity 80.3%; Score 500; DB 13; Length 375;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIAPKRYKANYCSGECENFTVSFWLRV 60
DB 267 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIAPKRYKANYCSGECENFTVSFWLRV 60
QY 61 PKVSASHL-----EAGPCTPTKMSPIINMLYFNKGKEQIITGKIPAMVVDRCGCS 109
DB 322 PHTHLVHQANPRGSAGPCCPTPKMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 375

RESULT 7
Q8UWD9 PRELIMINARY; PRT; 375 AA.
AC Q8UWD9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440862; AAL35276.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42667 MW; 57DDE49D3AA2978C CRC64;

Query Match
Best Local Similarity 79.5%; Score 495; DB 13; Length 375;
Matches 91; Conservative 1; Mismatches 12; Indels 10; Gaps 2;

QY 1 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIAPKRYKANYCSGECENFTVSFWLRV 60
DB 267 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIAPKRYKANYCSGECENFTVSFWLRV 60
QY 61 PKVSASHL-----EAGPCTPTKMSPIINMLYFNKGKEQIITGKIPAMVVDRCGCS 109
DB 322 PHTHLVHQANPRGSAGPCCPTPKMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 375

RESULT 8
Q8UWE0 PRELIMINARY; PRT; 375 AA.
AC Q8UWE0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
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DE Myostatin.
GN MSTN.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839.
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440861; AAL35275.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42817 MW; 1BA7FF5225C23620 CRC64;

Query Match
Best Local Similarity 79.1%; Score 493; DB 13; Length 375;
Matches 91; Conservative 1; Mismatches 12; Indels 10; Gaps 2;

QY 1 DFGLDGDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANCYSGCEFNFTVSFWLRV 60
DB 267 DFGLDGDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANCYSGCEFNFTVSFWLRV 60
QY 61 PKVSASHL-----EAGPCTPTKSPINMLYFNKGEOIYGKIPAMVVDRCGS 109
DB 322 PHTHLVHQANPRGSAGPCTPTKSPINMLYFNKGEOIYGKIPAMVVDRCGS 375

RESULT 9
Q8WNS6 PRELIMINARY; PRT; 375 AA.
AC Q8WNS6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN GDF8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913.
RN [1]
RP SEQUENCE FROM N.A.
RA Shibata M., Muramoto T., Aikawa K.;
RT "Genomic organization and sequence of the myostatin gene in bovine.";
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB076403; BAB79498.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb-propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42524 MW; 0EC27616C202F5E6 CRC64;

Query Match
Best Local Similarity 78.7%; Score 490; DB 6; Length 375;
Matches 90; Conservative 2; Mismatches 12; Indels 10; Gaps 2;

QY 1 DFGLDGDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANCYSGCEFNFTVSFWLRV 60
DB 267 DFGLDGDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANCYSGCEFNFTVSFWLRV 60
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DB 267 DFGLDGDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANCYSGCEFNFTVSFWLRV 321
QY 61 PKVSASHL-----EAGPCTPTKSPINMLYFNKGEOIYGKIPAMVVDRCGS 109
DB 322 PHTHLVHQANPRGSAGPCTPTKSPINMLYFNKGEOIYGKIPAMVVDRCGS 375

RESULT 10
Q95N11 PRELIMINARY; PRT; 185 AA.
AC Q95N11;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925.
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Pan Q., Chen H., Jin H., Li N.;
RT "Cloning of Intron 2 of the myostatin gene in goat.";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY032688; AAK49790.1; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb-propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
FT NON_TER 1 1
FT NON_TER 185 185
SQ SEQUENCE 185 AA; 20953 MW; 03675B386E9D64D4 CRC64;

Query Match
Best Local Similarity 78.2%; Score 487; DB 6; Length 185;
Matches 90; Conservative 2; Mismatches 7; Indels 16; Gaps 2;

QY 1 DFGLDGDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANCYSGCEFNFTVSFWLRV 60
DB 79 DFGLDGDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANCYSGCEFNFTVSFWLRV 130
QY 61 PKVSASHL-----EAGPCTPTKSPINMLYFNKGEOIYGKIPAMVVDRCG 107
DB 131 QKYPHTHLVHQANPRGSAGPCTPTKSPINMLYFNKGEOIYGKIPAMVVDRCG 185

RESULT 11
Q9MZ18 PRELIMINARY; PRT; 185 AA.
AC Q9MZ18;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940.
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Jin H., Li N.;
RT "Cloning of Intron 2 of the myostatin gene in sheep.";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF266758; AAF78069.1; -.
```

DR HSSP; P12643; 3BMP.  
DR InterPro: IPR001839; TGFb.  
DR InterPro: IPR001111; TGFb\_N.  
DR Pfam: PF00019; TGF-beta; 1.  
DR Pfam: PF00688; TGFb\_propeptide; 1.  
DR ProDom: PD000357; TGFb; 1.  
DR SMART: SM00204; TGFb; 1.  
DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
KW Glycoprotein.  
FT NON\_TER 1 1  
FT NON\_TER 185 185  
SQ SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;

Query Match 77.0%; Score 480; DB 6; Length 185;  
Best Local Similarity 77.4%; Pred. No. 3.2e-50;  
Matches 89; Conservative 2; Mismatches 8; Indels 16; Gaps 2;

OY 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNFTVSFWLRV 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 79 DFGLDGDVHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNFTVSFWLRV 130

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIYIGKIPAMVVDRCG 107  
| :|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 131 QKYPHTLVNQANPKGSAGPCCTPTKMSPINMLYFNKGKQIYIGKIPGMVVDRCG 185

RESULT 12  
O90YYO PRELIMINARY; PRT; 389 AA.

AC O90YYO;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Myostatin.  
OS Ictalurus punctatus (Channel catfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;  
OC Ictaluridae; Ictalurus.  
OX NCBI\_TaxID=7998;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kocabas A.M., Liu Z.J.;  
RT "Molecular characterization and expression of the myostatin gene from  
RT channel catfish (Ictalurus punctatus).";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: AF396747; AAK8466.1; -.  
DR InterPro: IPR001839; TGFb.  
DR InterPro: IPR001111; TGFb\_N.  
DR Pfam: PF00019; TGF-beta; 1.  
DR Pfam: PF00688; TGFb\_propeptide; 1.  
DR ProDom: PD000357; TGFb; 1.  
DR PROSITE: PS00250; TGF\_BETA\_1; UNKNOWN\_1.  
KW Glycoprotein.  
SQ SEQUENCE 389 AA; 43600 MW; 569FB952B7E9E173 CRC64;

Query Match 74.6%; Score 465; DB 13; Length 389;  
Best Local Similarity 73.0%; Pred. No. 4.7e-48;  
Matches 84; Conservative 8; Mismatches 7; Indels 16; Gaps 2;

OY 3 GIDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNFTVSFWLRVPK 62  
||||| :| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| :| :|  
Db 283 GIDCDENSESRCRCRYPLTVDFEFGWDWIIAPKRYKANYCSGECDFNFTVSFWLRVPK 334

OY 63 VSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIYIGKIPAMVVDRCGCS 109  
:|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 335 YPHTLVNKANPRGTAGPCTPTKMSPINMLYFNKGKQIYIGKIPSMVVDRCGCS 389

RESULT 13  
O90W05 PRELIMINARY; PRT; 385 AA.  
ID O90W05  
AC O90W05;

DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Myostatin.  
OS Sparus aurata (gilthead sea bream).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;  
OX NCBI\_TaxID=8175;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Maccatrozzo L., Bargelloni L., Radaelli G., Mascarello F.,  
RA Patarnello T.;  
RT "Characterization of the myostatin gene in the gilthead seabream,  
RT Sparus aurata: sequence, genomic structure, and expression pattern.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: AF258448; AAK53545.1; -.  
DR EMBL: AF258447; AAK53544.1; -.  
DR InterPro: IPR001839; TGFb.  
DR InterPro: IPR001111; TGFb\_N.  
DR Pfam: PF00019; TGF-beta; 1.  
DR Pfam: PF00688; TGFb\_propeptide; 1.  
DR ProDom: PD000357; TGFb; 1.  
DR PROSITE: PS00250; TGF\_BETA\_1; UNKNOWN\_1.  
KW Glycoprotein.  
SQ SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;

Query Match 74.5%; Score 464; DB 13; Length 385;  
Best Local Similarity 72.6%; Pred. No. 6.2e-48;  
Matches 85; Conservative 6; Mismatches 10; Indels 16; Gaps 2;

OY 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNFTVSFWLRV 60  
| ||||| :| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| :| :|  
Db 277 DSGLDCDENSPESRCRCRYPLTVDFEFGWDWIIAPKRYKANYCSGECEFNFTVSFWLRV 328

OY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIYIGKIPAMVVDRCGCS 109  
| :|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 329 QKYPHTLVNKANPRGSAGPCCTPTKMSPINMLYFNKRKQIYIGKIPSMVVDRCGCS 385

RESULT 14  
O9DDI8 PRELIMINARY; PRT; 373 AA.

AC O9DDI8;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Myostatin precursor.  
GN GDF-8.  
OS Salmo salar (Atlantic salmon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
OX NCBI\_TaxID=8030;  
RN [1]  
RP SEQUENCE FROM N.A.

RP Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.;  
RA "The two myostatin genes of Atlantic salmon (Salmo salar) are  
RT expressed in a variety of tissues.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.

RA Andersen O.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.

RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,  
RA Andersen O.;  
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are  
RL expressed in a variety of tissues.";  
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.





GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:03:23 ; Search time 12 Seconds  
(without alignments)  
376.743 Million cell updates/sec

Title: US-09-620-586b-19  
Perfect score: 623  
Sequence: 1 DFGLCDDEHSTESRCRYPL.....KEQIIVGKIPAMVVDRCGS 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	80.4	375	1	GDF8_CHICK
2	501	80.4	375	1	GDF8_HUMAN
3	501	80.4	375	1	GDF8_MELGA
4	501	80.4	375	1	GDF8_PIG
5	501	80.4	376	1	GDF8_MOUSE
6	501	80.4	376	1	GDF8_RAT
7	500	80.3	375	1	GDF8_SHEEP
8	495	79.5	375	1	GDF8_PAPHA
9	490	78.7	375	1	GDF8_BOVIN
10	468	75.1	374	1	GDF8_BRARE
11	467	75.0	405	1	GDFB_MOUSE
12	467	75.0	407	1	GDFB_HUMAN
13	420	67.4	345	1	GDFB_RAT
14	228	36.6	255	1	IHBB_MOUSE
15	219	35.2	391	1	IHBB_CHICK
16	218	35.0	349	1	IHBB_PIG
17	218	35.0	407	1	IHBB_HUMAN
18	218	35.0	408	1	IHBB_BOVIN
19	216.5	34.8	352	1	IHBC_MOUSE
20	215.5	34.6	424	1	IHBA_MOUSE
21	215.5	34.6	424	1	IHBA_PIG
22	215.5	34.6	424	1	IHBA_RAT
23	215.5	34.6	425	1	IHBA_BOVIN
24	215.5	34.6	425	1	IHBA_SHEEP
25	215.5	34.6	426	1	IHBA_HUMAN
26	214	34.3	350	1	DAF7_CAEL
27	213.5	34.3	351	1	IHBC_RAT
28	212.5	34.1	207	1	BMP6_RAT
29	212.5	34.1	513	1	BMP6_HUMAN
30	211.5	33.9	352	1	IHBC_HUMAN
31	211.5	33.9	426	1	IHBA_HORSE
32	210.5	33.8	510	1	BMP6_MOUSE
33	206.5	33.1	424	1	IHBA_CHICK

34	205	32.9	355	1	DVR1_BRARE	P35621 brachydanio
35	204.5	32.8	125	1	GDF6_MOUSE	P43028 mus musculus
36	204.5	32.8	436	1	GDF6_BOVIN	P55106 bos taurus
37	203.5	32.7	151	1	GDF7_MOUSE	P43029 mus musculus
38	203	32.6	393	1	BMP2_MOUSE	P49001 rattus norv
39	203	32.6	394	1	BMP2_MOUSE	P21274 mus musculus
40	203	32.6	395	1	BMP2_RABIT	O46564 oryctolagus
41	203	32.6	396	1	BMP2_DAMDA	O19006 dama dama (
42	203	32.6	396	1	BMP2_HUMAN	P12643 homo sapien
43	202	32.4	353	1	BMP2_CHICK	O90751 gallus gall
44	202	32.4	398	1	BMPA_XENLA	P25703 xenopus lae
45	202	32.4	398	1	BMPB_XENLA	P30884 xenopus lae

ALIGNMENTS

RESULT 1	
GDF8_CHICK	
ID GDF8_CHICK	STANDARD; PRT; 375 AA.
AC 042220;	
DT 15-JUL-1999 (Rel. 38, Created)	
DT 15-JUL-1999 (Rel. 38, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).	
GN GDF8 OR MSTN.	
OS Gallus gallus (Chicken).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC Gallus.	
OX NCBI_TaxID=9031;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=White leghorn; TISSUE=Skeletal muscle;	
RX MEDLINE=98024153; PubMed=9356471;	
RA McPherron A.C., Lee S.-J.;	
RT "Double muscling in cattle due to mutations in the myostatin gene.;"	
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).	
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL	
CC MUSCLE GROWTH.	
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).	
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	
CC	
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CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	
DR EMBL; AF019621; AAB86688.1; -	
DR HSSP; P18075; IBMF.	
DR InterPro; IPR001839; TGFb.	
DR InterPro; IPR001111; TGFb_N.	
DR Pfam; PF00019; TGF-beta; 1.	
DR Pfam; PF00688; TGFb_propeptide; 1.	
DR ProDom; PD000357; TGFb; 1.	
DR SMART; SM00204; TGFb; 1.	
DR PROSITE; PS00250; TGF_BETA_1; 1.	
KW Growth factor; Cytokine; Glycoprotein; Signal.	
FT SIGNAL	1 23
FT PROPEP	24 266
FT CHAIN	267 375
FT DISULFID	281 340
FT DISULFID	309 372
FT DISULFID	313 374
FT DISULFID	339 339
FT CARBOHYD	71 71
SQ SEQUENCE	375 AA; 42707 MW; DA732DB9426E4D4F CRC64;
Query Match	80.4%; Score 501; DB 1; Length 375;
Best Local Similarity	80.7%; Pred. No. 3.1e-48;

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANVCSGCECFNNFTVFWLRY 60  
 DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANVCSGCECF-----VFLQKY 321

OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109  
 DB 322 PHTHLVHQANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 375

## RESULT 2

GDF8\_HUMAN  
 ID GDF8\_HUMAN STANDARD; PRT; 375 AA.  
 AC 014793;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).  
 GN GDF8 OR MSTN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=98024153; PubMed=9356471;  
 RA McPherron A.C., Lee S.-J.;  
 RT "Double muscling in cattle due to mutations in the myostatin gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX MEDLINE=99061972; PubMed=9843994;  
 RA Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-Hikim I.,  
 RA Ma K., Ezzat S., Shen R., Lalani R., Asa S., Mamula M., Nair G.,  
 RA Ayer S., Bhasin S.;  
 RT "Organization of the human myostatin gene and expression in healthy  
 men and HIV-infected men with muscle wasting.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943(1998).  
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
 CC MUSCLE GROWTH.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: AF019627; AAB86694.1; -;  
 DR EMBL: AF104922; AAC96327.1; -;  
 DR HSSP: P18075; 1BMP.  
 DR Genew; HGNC:4223; GDF8.  
 DR MIM: 601788; -;  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR001111; TGFb\_N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor; Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT PROPEP 24 266 POTENTIAL.  
 FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.  
 FT DISULFID 281 340 BY SIMILARITY.  
 FT DISULFID 309 372 BY SIMILARITY.  
 FT DISULFID 313 374 BY SIMILARITY.

FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 71 71 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 375 AA; 42750 MW; EBF6129725E6AFA CRC64;

Query Match 80.4%; Score 501; DB 1; Length 375;  
 Best Local Similarity 80.7%; Pred. No. 3.1e-48;  
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANVCSGCECFNNFTVFWLRY 60  
 DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANVCSGCECF-----VFLQKY 321

OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109  
 DB 322 PHTHLVHQANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 375

## RESULT 3

GDF8\_MELGA  
 ID GDF8\_MELGA STANDARD; PRT; 375 AA.  
 AC 042221;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).  
 GN GDF8 OR MSTN.  
 OS Meleagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.  
 OX NCBI\_Taxid=9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=98024153; PubMed=9356471;  
 RA McPherron A.C., Lee S.-J.;  
 RT "Double muscling in cattle due to mutations in the myostatin gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).  
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
 CC MUSCLE GROWTH.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC -----  
 DR EMBL: AF019625; AAB86692.1; ALT\_INT.  
 DR HSSP: P18075; 1BMP.  
 DR InterPro; IPR001839; TGFb.  
 DR InterPro; IPR001111; TGFb\_N.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR Pfam; PF00688; TGFb\_propeptide; 1.  
 DR ProDom; PD000357; TGFb; 1.  
 DR SMART; SM00204; TGFb; 1.  
 DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
 KW Growth factor; Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT PROPEP 24 266 POTENTIAL.  
 FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.  
 FT DISULFID 281 340 BY SIMILARITY.  
 FT DISULFID 309 372 BY SIMILARITY.  
 FT DISULFID 313 374 BY SIMILARITY.  
 FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 71 71 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 375 AA; 42784 MW; D2AEAD732AEBAE77 CRC64;

Query Match 80.4%; Score 501; DB 1; Length 375;  
 Best Local Similarity 80.7%; Pred. No. 3.1e-48;  
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

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OY      1 DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRY 60
          |||||
Db      267 DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECF-----VFLQKY 321

OY      61 PKVSASHL-----EAGPCCPTPKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
          |
Db      322 PHTHLVHQANPRGSAGPCCPTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 4
GDF8_PIG          STANDARD;          PRT;          375 AA.
ID  GDF8_PIG
AC  018831;
DT  15-JUL-1999 (Rel. 38, Created)
DT  15-JUL-1999 (Rel. 38, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN  GDF8 OR MSTN.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Skeletal muscle;
RX  MEDLINE=98024153; PubMed=9356471;
RA  McPherron A.C., Lee S.-J.;
RT  "Double muscling in cattle due to mutations in the myostatin gene.";
RL  Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Duroc, Hampshire, Meishan, and Yorkshire;
RC  TISSUE=Skeletal muscle;
RA  Voelker G.R., Conroy J.C., Wheeler M.B.;
RT  "Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and
RT  Yorkshire pigs.";
RL  Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE OF 1-10 AND 36-375 FROM N.A.
RC  TISSUE=Muscle;
RA  Daneau I., Silversides D.W.;
RL  Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC  MUSCLE GROWTH.
CC  -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC  EMBL; AF019623; AAB86690.1; -.
DR  EMBL; AF188635; AAF02770.1; -.
DR  EMBL; AF188636; AAF02771.1; -.
DR  EMBL; AF188637; AAF02772.1; -.
DR  EMBL; AF188638; AAF02773.1; -.
DR  EMBL; AF033855; AAC08035.1; -.
DR  EMBL; AF093798; AAC62489.1; -.
DR  HSSP; P18075; 1BMP.
DR  InterPro; IPR001839; TGFb.
DR  InterPro; IPR001111; TGFb_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFb_propeptide; 1.
DR  ProDom; PD000357; TGFb; 1.
DR  SMART; SM00204; TGFb; 1.
DR  ProSite; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Cytokine; Glycoprotein; Signal.
FT  SIGNAL 1 23 POTENTIAL.

```

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FT  PROPEP 24 266 POTENTIAL.
FT  CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT  DISULFID 281 340 BY SIMILARITY.
FT  DISULFID 309 372 BY SIMILARITY.
FT  DISULFID 313 374 BY SIMILARITY.
FT  DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT  CARBOHYD 71 71 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ  SEQUENCE 375 AA; 42791 MW; 0F658685EFDA3418 CRC64;

Query Match      80.4%; Score 501; DB 1; Length 375;
Best Local Similarity 80.7%; Pred. No. 3.1e-48;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY      1 DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFNNFTVSFWLRY 60
          |||||
Db      267 DFGLDCEHSTESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECF-----VFLQKY 321

OY      61 PKVSASHL-----EAGPCCPTPKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
          |
Db      322 PHTHLVHQANPRGSAGPCCPTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 5
GDF8_MOUSE          STANDARD;          PRT;          376 AA.
ID  GDF8_MOUSE
AC  008689;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN  GDF8 OR MSTN.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CD-1; TISSUE=Skeletal muscle;
RX  MEDLINE=97284412; PubMed=9139826;
RA  McPherron A.C., Lawler A.M., Lee S.-J.;
RT  "Regulation of skeletal muscle mass in mice by a new TGF-beta
RT  superfamily member.";
RL  Nature 387:83-90(1997).
CC  -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC  MUSCLE GROWTH.
CC  -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC  -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
CC  SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
CC  -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-CONITUM IN
CC  ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE
CC  MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,
CC  DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
CC  CONTINUES IN ADULTHOOD.
CC  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC  or send an email to license@isb-sib.ch).
-----
CC  EMBL; U84005; AAC53167.1; -.
DR  HSSP; P18075; 1BMP.
DR  MGI; MGI:95691; Gdf8.
DR  InterPro; IPR001839; TGFb.
DR  InterPro; IPR001111; TGFb_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFb_propeptide; 1.
DR  ProDom; PD000357; TGFb; 1.
DR  SMART; SM00204; TGFb; 1.
DR  ProSite; PS00250; TGF_BETA_1; 1.

```



KW Growth factor; Cytokine; Glycoprotein; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT PROPEP 25 267 POTENTIAL.  
FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.  
FT DISULFID 282 341 BY SIMILARITY.  
FT DISULFID 310 373 BY SIMILARITY.  
FT DISULFID 314 375 BY SIMILARITY.  
FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 376 AA; 42921 MW; 3E19814DD62C08BE CRC64;  
  
Query Match  
Best Local Similarity 80.4%; Score 501; DB 1; Length 376;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;  
  
QY 1 DFGLDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCEFNFTVSEWLRV 60  
|||||  
Db 268 DFGLDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCEFNFTVSEWLRV 60  
|||||  
QY 61 PKVSASHL-----EAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 109  
|  
Db 323 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 376  
|||||  
  
RESULT 6  
GDF8\_RAT STANDARD; PRT; 376 AA.  
ID GDF8\_RAT  
AC 035312;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).  
GN GDF8 OR MSTN.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=98024153; PubMed=9356471;  
RA McPherron A.C., Lee S.-J.;  
RT "Double muscling in cattle due to mutations in the myostatin gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).  
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
CC MUSCLE GROWTH.  
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC  
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CC  
CC -----  
CC EMBL; AF019624; AAB86691.1; -.  
DR HSSP; P18075; 1BMP.  
DR InterPro; IPR001839; TGFb.  
DR InterPro; IPR001111; TGFb\_N.  
DR Pfam; PF00019; TGF-beta; 1.  
DR Pfam; PF00688; TGFb-propeptide; 1.  
DR ProDom; PD000357; TGFb; 1.  
DR SMART; SM00204; TGFb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
KW Growth factor; Cytokine; Glycoprotein; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT PROPEP 25 267 POTENTIAL.  
FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.  
FT DISULFID 282 341 BY SIMILARITY.  
FT DISULFID 310 373 BY SIMILARITY.  
FT DISULFID 314 375 BY SIMILARITY.

FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 376 AA; 42829 MW; 933043D8C8C3294B CRC64;  
  
Query Match  
Best Local Similarity 80.4%; Score 501; DB 1; Length 376;  
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;  
  
QY 1 DFGLDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCEFNFTVSEWLRV 60  
|||||  
Db 268 DFGLDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCEFNFTVSEWLRV 60  
|||||  
QY 61 PKVSASHL-----EAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 109  
|  
Db 323 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIYGKIPAMVVDRCGCS 376  
|||||  
  
RESULT 7  
GDF8\_SHEEP STANDARD; PRT; 375 AA.  
ID GDF8\_SHEEP  
AC 018830;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).  
GN GDF8 OR MSTN.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=98024153; PubMed=9356471;  
RA McPherron A.C., Lee S.-J.;  
RT "Double muscling in cattle due to mutations in the myostatin gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).  
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
CC MUSCLE GROWTH.  
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; AF019622; AAB86689.1; -.  
DR HSSP; P18075; 1BMP.  
DR InterPro; IPR001839; TGFb.  
DR InterPro; IPR001111; TGFb\_N.  
DR Pfam; PF00019; TGF-beta; 1.  
DR Pfam; PF00688; TGFb-propeptide; 1.  
DR ProDom; PD000357; TGFb; 1.  
DR SMART; SM00204; TGFb; 1.  
DR PROSITE; PS00250; TGF\_BETA\_1; 1.  
KW Growth factor; Cytokine; Glycoprotein; Signal.  
FT SIGNAL 1 23 POTENTIAL.  
FT PROPEP 24 266 POTENTIAL.  
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.  
FT DISULFID 281 340 BY SIMILARITY.  
FT DISULFID 309 372 BY SIMILARITY.  
FT DISULFID 313 374 BY SIMILARITY.  
FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 375 AA; 42827 MW; 1C36F383BB11241 CRC64;  
  
Query Match 80.3%; Score 500; DB 1; Length 375;







```

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD,
CC 'INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING
CC TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT
CC DENTAL PULP AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED
CC DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE
CC TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB
CC BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED
CC IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM,
CC RETINA AND SPECIFIC REGIONS OF THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF100906; AAC72853.1; -.
CC EMBL; AF100904; AAC72853.1; JOINED.
CC EMBL; AF100905; AAC72853.1; JOINED.
CC EMBL; AF028337; AAF21633.1; -.
CC EMBL; AF028335; AAF21633.1; JOINED.
CC EMBL; AF028336; AAF21633.1; JOINED.
CC EMBL; AF092734; AAD05267.1; -.
CC HSSP; P18075; IBMP.
CC MGD; MG1:1338027; Gdf11.
CC InterPro; IPR001839; TGFb.
CC InterPro; IPR001111; TGFb_N.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGFb_propeptide; 1.
CC ProDom; PD000357; TGFb; 1.
CC SMART; SM00204; TGFb; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC KW SIGNAL 1 20 POTENTIAL.
CC FT PROPEP 21 296 BY SIMILARITY.
CC FT CHAIN 297 405 GROWTH/DIFFERENTIATION FACTOR 11.
CC FT DOMAIN 29 39 POLY-ALA.
CC FT DOMAIN 208 213 POLY-GLY.
CC FT DISULFID 311 370 BY SIMILARITY.
CC FT DISULFID 339 402 BY SIMILARITY.
CC FT DISULFID 343 404 BY SIMILARITY.
CC FT DISULFID 369 369 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 75 75 E -> G (IN REF. 3).
CC FT CONFLICT 171 171 T -> N (IN REF. 2).
CC SQ SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;

Query Match 75.0%; Score 467; DB 1; length 405;
Best Local Similarity 71.8%; Pred. No. 2e-44;
Matches 84; Conservative 8; Mismatches 9; Indels 16; Gaps 2;

QY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNFTVSFWLRV 60
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 NLGLCDEHSSSESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEY-----MFM 348

QY 61 PKYSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGS 109
: || :|| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 OKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQIITYGKIPGMVVVDRCGS 405

RESULT 12
GDFB_HUMAN STANDARD; PRT; 407 AA.
ID GDFB_HUMAN 095390; 09UID1; 09UID2;
AC 095390; 09UID1; 09UID2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein
DE 11).

```

```

GN  GDF11 OR BMP11.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Fetal brain;
RX  MEDLINE=99177155; PubMed=10075854;
RA  Gamber L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
RA  Rosen V.;
RT  "A novel BMP expressed in developing mouse limb, spinal cord, and tail
RT  bud is a potent mesoderm inducer in Xenopus embryos.";
RL  Dev. Biol. 208:222-232(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99318097; PubMed=10391213;
RA  McPherron A.C., Lawler A.M., Lee S.-J.;
RT  "Regulation of anterior/posterior patterning of the axial skeleton by
RT  growth/differentiation factor 11.";
RL  Nat. Genet. 22:260-264(1999).
CC  -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
CC  IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
CC  PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC  TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC  -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC  -----
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CC  -----
DR  EMBL; AF100907; AAC72852.1; -
DR  EMBL; AF028333; AAF21630.1; -
DR  EMBL; AF028334; AAF21631.1; -
DR  HSSP; P18075; 1BMP.
DR  Genew; HGNC:4216; GDF11.
DR  MIM; 603936; -
DR  InterPro; IPR001839; TGFb.
DR  InterPro; IPR001111; TGFb_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFb-propeptide; 1.
DR  ProDom; PD000357; TGFb; 1.
DR  SMART; SM00204; TGFb; 1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Cytokine; Glycoprotein; Signal.
FT  SIGNAL 1 24 POTENTIAL.
FT  PROPEP 25 298 BY SIMILARITY.
FT  CHAIN 299 407 GROWTH/DIFFERENTIATION FACTOR 11.
FT  DOMAIN 29 41 POLY-ALA.
FT  DOMAIN 210 215 POLY-GLY.
FT  DISULFID 313 372 BY SIMILARITY.
FT  DISULFID 341 404 BY SIMILARITY.
FT  DISULFID 345 406 BY SIMILARITY.
FT  DISULFID 371 371 INTERCHAIN (BY SIMILARITY).
FT  CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  SEQUENCE 407 AA; 45090 MW; E8FF48E363635BA8 CRC64;

Query Match 75.0%; Score 467; DB 1; Length 407;
Best Local Similarity 71.8%; Pred. No. 2e-44;
Matches 84; Conservative 8; Mismatches 9; Indels 16; Gaps 2

OY 1 DFGLDCEHSHESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRY 60
   : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 NLGLDCDEHSHESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCGCEY-----MFM 350
   : || :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 PKVSASHL-----EAGPCCTPTKMSPIIMLYENGKEQIITYGKIPAWVYDRCGCS 109
   | :|| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```











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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:09:33 ; Search time 43 Seconds  
(without alignments)  
243.690 Million cell updates/sec

Title: US-09-620-586B-19  
Perfect score: 623  
Sequence: 1 DFGLCDDEHSTESRCCRYPL.....KEQIIYGKIPAMVYDRCGCS 109

Scoring table: BLOSUM62  
Gapop. 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	230	36.9	370	2	I51199	activin beta B sub
2	228	36.6	255	2	I48235	inhibin beta-B cha
3	228	36.6	411	2	B41398	inhibin beta-B cha
4	218	35.0	349	1	WEPGBB	inhibin beta-B cha
5	218	35.0	407	1	A40150	inhibin beta-B cha
6	218	35.0	408	2	S50899	betab inhibin prec
7	217.5	34.9	115	2	PN0506	activin beta B-2 c
8	217.5	34.9	393	2	I50103	activin beta B - z
9	216.5	34.8	115	2	PN0505	activin beta B-1 c
10	216.5	34.8	352	2	JC5366	activin beta C - m
11	216.5	34.8	352	2	S70580	activin beta C pre
12	215.5	34.6	424	1	WEPGBA	inhibin beta-A cha
13	215.5	34.6	424	1	S31440	inhibin beta-A cha
14	215.5	34.6	424	1	B40905	inhibin beta-A cha
15	215.5	34.6	425	1	S50898	inhibin beta-A cha
16	215.5	34.6	425	2	I47072	inhibin beta-A cha
17	215.5	34.6	426	1	B24248	inhibin beta-A cha
18	214.5	34.4	367	2	JC4151	activin beta-A cha
19	214	34.3	350	2	T25451	activin beta D cha
20	212.5	34.1	207	2	S37618	transforming growt
21	212.5	34.1	513	1	BMH06	vgr protein - rat
22	211.5	33.9	352	2	JC2466	bone morphogenetic
23	210.5	33.8	510	2	A54798	inhibin beta-C cha
24	206	33.1	373	2	PW0042	Vg-1-related prote
25	204.5	32.8	125	2	S43295	bone morphogenetic
26	204.5	32.8	436	2	B54542	cartilage-derived
27	203.5	32.7	151	2	S43296	bone morphogenetic
28	203	32.6	393	2	S37073	bone morphogenetic
29	203	32.6	394	2	S45355	bone morphogenetic

30	203	32.6	396	1	BMH02	bone morphogenetic
31	202	32.4	353	2	I50607	bone morphogenetic
32	202	32.4	398	2	JH0688	bone morphogenetic
33	202	32.4	398	2	JH0687	bone morphogenetic
34	201.5	32.3	413	2	JC4862	activin beta-A cha
35	197.5	31.7	452	2	I49542	bone morphogenetic
36	197.5	31.7	454	1	BMH05	bone morphogenetic
37	197.5	31.7	461	2	S52408	SPDVR1 protein - s
38	197	31.6	366	2	A46607	growth/differentia
39	195.5	31.4	313	2	I51284	bone morphogenetic
40	195.5	31.4	360	2	A29619	Vg1 embryonic grow
41	195	31.3	360	2	I53032	bone morphogenetic
42	195	31.3	366	2	A45402	transforming growt
43	194.5	31.2	402	2	A45056	osteogenic protein
44	194.5	31.2	426	2	JH0690	bone morphogenetic
45	194.5	31.2	495	2	S43294	bone morphogenetic

ALIGNMENTS

RESULT 1  
I51199  
activin beta B subunit - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C;Accession: I51199  
R;Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melt  
Dev. Biol. 157, 474-483, 1993  
A;Title: Expression of activin mRNA during early development in Xenopus laevis.  
A;Reference number: I51199; MUID:93273083; PMID:8500654  
A;Accession: I51199  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-370 <DOH>  
A;Cross-references: GB:S61773; NID:g386027; PIDN:AAB26863.1; PID:g386028  
C;Superfamily: inhibin

Query Match 36.9%; Score 230; DB 2; Length 370;  
Best Local Similarity 37.4%; Pred. No. 2.7e-17;  
Matches 46; Conservative 17; Mismatches 36; Indels 24; Gaps 4;

QY 3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGEGCFNNFTVSFWLRVP 61  
Db 256 GLECDGHT--NLCCRQOXYIDFRLIGMNDWIIAPAGYYGNYCEGSCP-----AYLAGVP 307  
QY 62 KVSASHLEA-----GPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVYDRG 106  
Db 308 GSASSFHTAVVNQYRMGLNPGTVNSSCIPTKLSTMSMLYFDDEYNIVKRDVPMIIVDEC 367  
QY 107 GCS 109  
Db 368 GCA 370

RESULT 2  
I48235  
inhibin beta-B chain - mouse (fragment)  
N;Alternate names: activin bb chain  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 01-Aug-1997 #text\_change 16-Jul-1999  
C;Accession: I48235; I48266; S31441  
R;Ritvos, O.; Tuuri, T.; Brama, M.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F.  
Mech. Dev. 50, 229-245, 1995  
A;Title: Activin disrupts epithelial branching morphogenesis in developing glandular  
A;Reference number: I48235; MUID:95344997; PMID:7619733  
A;Accession: I48235  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-234 <RES>  
A;Cross-references: EMBL:X83376; NID:g603571; PIDN:CAA58290.1; PID:g603572  
R;Albano, R.M.; Groome, N.; Smith, J.C.  
Development 117, 711-723, 1993





A;Accession: A40156  
A;Molecule type: mRNA  
A;Residues: 22-46, 'A', 48-407 <FEN>  
A;Cross-references: GB:M31632  
A;Experimental source: testis  
R;Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N.  
Biochim. Biophys. Acta 1039, 135-141, 1990  
A;Title: Purification and characterization of recombinant human activin B.  
A;Reference number: S10751; MUID:90304183; PMID:2364091  
A;Accession: S10751  
A;Molecule type: protein  
A;Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>  
C;Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.  
bin beta-A and beta-B, respectively.  
C;Genetics:  
A;Gene: GDB:INHBB  
A;Cross-references: GDB:119347; OMIM:147390  
A;Map position: 2cen-2q13  
C;Superfamily: inhibin  
C;Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-292/Domain: propeptide #status predicted <PRO>  
F;293/Product: inhibin beta-B chain #status predicted <MAT>  
F;93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 218; DB 1; Length 407;  
 Best Local Similarity 35.8%; Pred. No. 6e-16;  
 Matches 44; Conservative 18; Mismatches 37; Indels 24; Gaps 4;

```

QY      3 GLDCDEHSTERCRCRYPLTVDFEAFGM-DWIIAPKRYKANCSCGECEENNFTVTSFWLRYP 61
      11::: : - : 111 : 11 111111 1 111 1 : 11
Db     293 GLECDGRT--NLCCRQGFIDFRLLIGMDWIIAPTGYGYNCYCESCP-----AYLAGVP 344

```

```
QY      62 KVSASHLEA-----GPCCTPTKMSPIINMLYFNKGEOIITYGKIPAMVVDRC 106  
       ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db     345 GSASSFHTAVVNQYRMGLNPGTVNSCCIPTKLSTMSMLYFDDEVENIVKRDPVNMIVEEC 404
```

QY	107	GCS	109
		:	
Db	405	GCA	407

RESULT 6  
S50899

betab inhibin precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-1999  
C;Accession: S50899  
R;Thompson, D.A.; Cronin, C.N.; Martin, F.  
Eur. J. Biochem. 226, 751-764, 1994  
A;Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B)-  
Y DNase I footprinting.  
A;Reference number: S50897; MUID:95112839; PMID:7813465  
A;Accession: S50899  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-408 <THO>  
A;Cross-references: EMBL:U16240  
C;Genetics:  
A;Introns: 151/1  
C;Superfamily: inhibin

Query Match	35.0%;	Score 218;	DB 2;	Length 408;
Best Local Similarity	35.8%;	Pred. No. 6e-16;		
Matches 44;	Conservative 18;	Mismatches 37;	Indels 24;	Gaps 4;

QY 3 GLDDEHSTESRCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCECFENFTVSFWLRVP 61  
 1111 : : 111 1111111 1111 : 11  
 Db 294 GLECDGRT--NLCCRQGFIDFRLIGWMDWIIAPTYGYGNYCEGSCP-----AYLAGVP 34

```

QY      62 KVSASHLEA-----GPCTPTKMSPIMLYENGKQIIFYGKIPAMVVDRC 106
      ::-|  || |||:| ::|||:| :| :| :|:| :|
Db      346 GSASSFHTAVVNOYRMRGLPCTVNSCCIPTKLSTMSMLYFDEDEVNIIVKRDVPMNIVEEC 405

```

QY	107	GCS	109
		:	
Db	406	GCA	408

RESULT 7  
PN0506  
activin beta B-2 chain - goldfish (fragment)

N/A;Accession: P05006  
 C;Species: Carassius auratus (goldfish)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C;Accession: P05006  
 R;Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.  
 Biochem. Biophys. Res. Commun. 193, 711-717, 1993  
 A;Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural  
 A;Reference number: P05004; MUID:93290666; PMID:8512569  
 A;Accession: P05006  
 A;Molecule type: DNA  
 A;Residues: 1-115 <GEW>  
 C;Superfamily: inhibitor

Query Match	34.98;	Score 217.5;	DB 2;	Length 115;
Best Local Similarity	36.98;	Pred. No. 1.9e-16;		
Matches 45;	Conservative 15;	Mismatches 39;	Indels 23;	Gaps 4;

QY 3 GLDDEHSTESRCCRYPLTVDFEAFGW-DWIAPKRRKANYSGECEFFNNFTVSFWLRVP 61  
||:|| : ||| :|| ||||||| | ||| | : ||  
Db 1 GLECD-GTNGGLCCROQFYIDFRLLIGMNDWIIATPAGYYGNICEGSCP-----AFLAGVP 53

```
QY      62 KVSASHLEA-----GPECTPTKMSPIINMLYFNGKEOIYYGKIPAMVVDRC 106
      : : |      | | | | : : | | : : | | : : |
Db      54 GSASSFHTAVVNOYRMGMSPGSVNSCCITPKLSTMSMLYFEDDEYNIIVKRDVPNMIYECC 113
```

QY	107	GC	108
Db	114	GC	115

RESULT 8  
I50103

activin beta B - zebra fish  
C;Species: Brachydanio rerio (zebra fish)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C;Accession: I50103  
R;Wittbrodt, J.; Rosa, F.M.  
Genes Dev. 8, 1448-1462, 1994  
A;Title: Disruption of mesoderm and axis formation in fish by ectopic expression of a  
A;Reference number: I50103; MUID:95011555; PMID:7926744  
A;Accession: I50103  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA  
A;Residues: 1-393 <WIT>  
A;Cross-references: EMBL:X76051; NID:g516356; PIDN:CAA53636.1; PID:g516357  
C;Genetics:  
A;Gene: Zactbetab  
C;Superfamily: inhibin

Query Match	34.98;	Score 217.5;	DB 2;	Length 393;
Best Local Similarity	35.88;	Pred. No. 6.6e-16;		
Matches 44; Conservative	18;	Mismatches 38;	Indels 23;	Gaps 4;

QY 3 GLDDEHSTESRCRYPLTVDFEAFGW-DWIIAPKRYKANYSGECEFFNNFTVSFWLRVP 61  
 ||:|:| :| | | | | | | | | | :| :|  
 Db 278 GLECDGNN-GGLCCRQFYIDFRLLIGWMDWIIAPAGYGYGNYCEGSCP-----AYMAGVP 330

```

QY      62 KVSASHLEA-----GPCCTPTKMSPIINMLYENGKEQIIYGKIPAMVVDRC 106
      ::!  |  ||||| : : ||| : |
Db     331 GSASSFHTAVVNOYRMKGMSPGVSVNCCIPTKLSTMSMLYFDEEYINIVKRDVPNMLYECC 390

```

QY	107	GCS	109
		:	
Db	391	GCA	393

QY	107	GCS	109
		:	
Db	406	GCA	408

RESULT 7  
PN0506  
activin beta B-2 chain - goldfish (fragment)

N/A;Accession: P05006  
 C;Species: Carassius auratus (goldfish)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C;Accession: P05006  
 R;Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.  
 Biochem. Biophys. Res. Commun. 193, 711-717, 1993  
 A;Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural  
 A;Reference number: P05004; MUID:93290666; PMID:8512569  
 A;Accession: P05006  
 A;Molecule type: DNA  
 A;Residues: 1-115 <GEW>  
 C;Superfamily: inhibitor

Query Match	34.98;	Score 217.5;	DB 2;	Length 115;
Best Local Similarity	36.98;	Pred. No. 1.9e-16;		
Matches 45;	Conservative 15;	Mismatches 39;	Indels 23;	Gaps 4;

QY 3 GLDDEHSTESRCCRYPLTVDFEAFGW-DWIAPKRRKANYSGECEFFNNFTVSFWLRVP 61  
||:|| : ||| :|| ||||||| | ||| | : ||  
Db 1 GLECD-GTNGGLCCROQFYIDFRLLIGMNDWIIATPAGYYGNICEGSCP-----AFLAGVP 53

```
QY      62 KVSASHLEA-----GPECTPTKMSPINMLYFNGKEQI IYGKIPAMVVDRC 106
      : : |      | | | | : : | | : : | | : : |
Db      54 GSASSFHTAVVNOYRMGMSGVNSCCPTKLTSMMLYFEDDEYNIIVKRDVPNM IYEEC 113
```

QY	107	GC	108
Db	114	GC	115

RESULT 8  
I50103

activin beta B - zebra fish  
C;Species: Brachydanio rerio (zebra fish)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C;Accession: I50103  
R;Wittbrodt, J.; Rosa, F.M.  
Genes Dev. 8, 1448-1462, 1994  
A;Title: Disruption of mesoderm and axis formation in fish by ectopic expression of a  
A;Reference number: I50103; MUID:95011555; PMID:7926744  
A;Accession: I50103  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA  
A;Residues: 1-393 <WIT>  
A;Cross-references: EMBL:X76051; NID:g516356; PIDN:CAA53636.1; PID:g516357  
C;Genetics:  
A;Gene: ZactbetaB  
C;Superfamily: inhibin

Query Match	34.98;	Score 217.5;	DB 2;	Length 393;
Best Local Similarity	35.88;	Pred. No. 6.6e-16;		
Matches 44; Conservative	18;	Mismatches 38;	Indels 23;	Gaps 4;

QY 3 GLDDEHSTESRCRYPLTVDFEAFGW-DWIIAPKRYKANYSGECEFFNNFTVSFWLRVP 61  
 ||:||: ||| :|| ||||||| | ||| | ||  
 Db 278 GLECDGNN-GGLCCRQFYIDFRLLIGWMDWIIAPAGYGYGNYCEGSCP-----AYMAGVP 330

```
QY      62 KVSASHLEA-----GPCCTPTKMSPIINMLYENGKEQIIYGKIPAMVVDRC 106
       ::! |          |||:::||||: : |: :}||: |
Db     331 GSASSEHTAVVNQYRMKGMSGVSNSCCIPTKLSTMSMLYFDEEYNIVKRDPVPMIYECC 390
```

QY	107	GCS	109
		:	
Db	391	GCA	393

RESULT 9  
PN0505  
activin beta B-1 chain - goldfish (fragment)  
N:Alternate names: gact 2  
C:Species: Carassius auratus (goldfish)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PN0505  
R:Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.  
Biochem. Biophys. Res. Commun. 193, 711-717, 1993  
A:Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con  
A:Reference number: PN0504; MUID:93290666; PMID:8512569  
A:Accession: PN0505  
A:Molecule type: DNA  
A:Residues: 1-115 <GEN>  
C:Superfamily: Inhibin

Query Match 34.8%; Score 216.5; DB 2; Length 115;  
Best Local Similarity 37.0%; Pred. No. 2.4e-16;  
Matches 44; Conservative 19; Mismatches 39; Indels 17; Gaps 5;

OY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGEC-----EF 49  
||:|:| : ||| :|| ||||| | ||| |  
Db 1 GLECD-GTNGGLCCRQEQFYIDFRLIGWMDWIIAPAGYGNICEGSCPAYMAGVPGSASSF 59  
C:Accession: JC5366  
R:Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.  
Biochem. Biophys. Res. Commun. 231, 655-661, 1997  
A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit  
A:Reference number: JC5366; MUID:97224404; PMID:9070865  
A:Accession: JC5366  
A:Molecule type: DNA  
A:Residues: 1-352 <FAN>  
A:Cross-references: GB:U95962  
C:Comment: Activin beta C and beta E form a distinct subset of related activins.  
C:Genetics:  
A:Introns: 105/3  
C:Superfamily: inhibin

RESULT 10  
JC5366  
activin beta C - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 26-Aug-1999  
C:Accession: JC5366  
R:Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.  
Biochem. Biophys. Res. Commun. 231, 655-661, 1997  
A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit  
A:Reference number: JC5366; MUID:97224404; PMID:9070865  
A:Accession: JC5366  
A:Molecule type: DNA  
A:Residues: 1-352 <FAN>  
A:Cross-references: GB:U95962  
C:Comment: Activin beta C and beta E form a distinct subset of related activins.  
C:Genetics:  
A:Introns: 105/3  
C:Superfamily: inhibin

Query Match 34.8%; Score 216.5; DB 2; Length 352;  
Best Local Similarity 37.3%; Pred. No. 7.5e-16;  
Matches 44; Conservative 17; Mismatches 44; Indels 13; Gaps 4;

OY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGECFN-----NFTVSF 56  
||:|:| : ||| :|| ||||| | ||| |  
Db 237 GIDCQGG--RMCCKRQEFFVDFREIGWMDWIIQPEGYAMNFCGTGQCPPLHVAGMPGISASF 294  
C:Accession: S70580  
R:lan, A.L.; Nishimori, K.; Matzuk, M.M.  
Biochim. Biophys. Acta 1307, 145-148, 1996  
A:Title: Structural analysis of the mouse activin beta-C gene.  
A:Reference number: S70580; MUID:96283807; PMID:8679697

RESULT 11  
S70580  
activin beta C precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S70580  
R:lan, A.L.; Nishimori, K.; Matzuk, M.M.  
Biochim. Biophys. Acta 1307, 145-148, 1996  
A:Title: Structural analysis of the mouse activin beta-C gene.  
A:Reference number: S70580; MUID:96283807; PMID:8679697

A:Accession: S70580  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-352 <LAU>  
A:Cross-references: EMBL:U40772  
C:Genetics:  
A:Introns: 106/1  
C:Superfamily: inhibin

Query Match 34.8%; Score 216.5; DB 2; Length 352;  
Best Local Similarity 36.4%; Pred. No. 7.5e-16;  
Matches 43; Conservative 17; Mismatches 45; Indels 13; Gaps 4;

OY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGECFN-----NFTVSF 56  
||:|:| : ||| :|| ||||| | ||| |  
Db 237 GIDC--QGASRMCCKRQEFFVDFREIGWMDWIIQPEGYAMNFCGTGQCPPLHVAGMPGISASF 294  
C:Accession: A60087; I48265; S31440  
R:Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack,  
Development 110, 435-443, 1990  
A:Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia  
A:Reference number: A60087; MUID:92155098; PMID:2133547  
A:Accession: A60087  
A:Molecule type: protein

RESULT 12

WFPGBA  
inhibin beta-A chain precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 18-Jun-1999  
C:Accession: A01393  
R:Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R  
Nature 318, 659-663, 1985  
A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precurs  
A:Reference number: A93371; MUID:86092207; PMID:2417121  
A:Accession: A01393  
A:Molecule type: mRNA  
A:Residues: 1-424 <MAS>  
A:Cross-references: GB:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003  
C:Comment: The source of this protein is ovarian follicular fluid.  
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypep  
ifferent forms of inhibin have been isolated (A and B) that differ in the amino-termi  
C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of fol  
C:Superfamily: inhibin  
C:Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad  
F:1-20/Domain: signal sequence #status predicted <PRO>  
F:21-308/Domain: propeptide #status predicted <SIG>  
F:309-424/Product: inhibin beta-A chain #status predicted <MAT>  
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.6%; Score 215.5; DB 1; Length 424;  
Best Local Similarity 36.7%; Pred. No. 1.2e-15;  
Matches 44; Conservative 21; Mismatches 38; Indels 17; Gaps 4;

OY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGEC-----EF 49  
||:|:| : ||| :|| ||||| | ||| |  
Db 309 GLECD--GKVNICKCKQEFVSEFKDIGWMDWIIAPSGYHANYCEGECPSHIAGTSGSSLSF 366  
C:Accession: A60087; I48265; S31440  
R:Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack,  
Development 110, 435-443, 1990  
A:Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia  
A:Reference number: A60087; MUID:92155098; PMID:2133547  
A:Accession: A60087  
A:Molecule type: protein

RESULT 13

S31440  
inhibin beta-A chain - mouse  
N:Alternate names: activin A; mesoderm-inducing factor WEHI-MIF  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A60087; I48265; S31440  
R:Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack,  
Development 110, 435-443, 1990  
A:Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia  
A:Reference number: A60087; MUID:92155098; PMID:2133547  
A:Accession: A60087  
A:Molecule type: protein



